

(26) DNA228201 (TAT116)

The malignant cells of 13/16 colorectal adenocarcinomas are positive for TAT116 expression. Additionally, 9/10 metastatic adenocarcinomas are positive for expression. Expression is also observed in the basal portions of normal colonic crypts.

(27) DNA247488 (TAT189)

5 The malignant cells of 13/16 colorectal adenocarcinomas are positive for TAT189 expression. Additionally, 9/10 metastatic adenocarcinomas are positive for expression. Expression is also observed in the basal portions of normal colonic crypts.

(28) DNA236538 (TAT190)

10 The malignant cells of 13/16 colorectal adenocarcinomas are positive for TAT190 expression. Additionally, 9/10 metastatic adenocarcinomas are positive for expression. Expression is also observed in the basal portions of normal colonic crypts.

(29) DNA247489 (TAT191)

15 The malignant cells of 13/16 colorectal adenocarcinomas are positive for TAT191 expression. Additionally, 9/10 metastatic adenocarcinomas are positive for expression. Expression is also observed in the basal portions of normal colonic crypts.

(30) DNA228994 (TAT124)

Thirteen of 61 case of non small cell lung carcinoma are positive for expression of TAT124. Expression level in these positive tumor samples is significantly higher than in normal adult tissues.

(31) DNA231542 (TAT100)

20 *In situ* analysis performed as described above evidences significantly upregulated expression in human glioma and glioblastoma tissues as compared to normal brain (and other) tissue.

(32) DNA231542-1 (TAT284)

In situ analysis performed as described above evidences significantly upregulated expression in human glioma and glioblastoma tissues as compared to normal brain (and other) tissue.

25 (33) DNA231542-2 (TAT285)

In situ analysis performed as described above evidences significantly upregulated expression in human glioma and glioblastoma tissues as compared to normal brain (and other) tissue.

(34) DNA297393 (TAT285-1)

30 *In situ* analysis performed as described above evidences significantly upregulated expression in human glioma and glioblastoma tissues as compared to normal brain (and other) tissue.

(35) DNA236534 (TAT102)

35 Expression of TAT102 is seen in 14 of 15 ovarian epithelial malignancies (adenocarcinoma, epithelial surface tumors, endometrioid Ca). Also, 8 of 9 endometrial adenocarcinomas of the uterus express TAT102. Moreover, expression of TAT102 is seen in 24 of 27 non-small cell lung cancers, positive cases include squamous and adenocarcinomas. Expression in these tumor tissues is significantly higher than in their normal tissue counterparts.

(36) DNA246430 (TAT109)

Fourteen of 92 breast tumor samples are positive for TAT109 expression. Expression in all normal tissues is undetectable.

(37) DNA264454 (TAT106)

Expression of TAT106 is observed in 38/88 breast tumors. Expression in normal breast tissue is weak or undetectable.

(38) DNA98565 (TAT145)

Positive signal for TAT145 was observed in most gliomas, glioblastomas, some melanomas, and normal brain (primarily localized to astrocytes). The signal intensity in the glioblastomas appeared to be greater than that in normal astrocytes. While the majority of glioma and glioblastoma samples tested were positive for TAT145 expression, the majority of normal brain samples tested were negative for such expression.

(39) DNA246435 (TAT152)

Positive signal for TAT152 was observed in most glioblastomas, some melanomas, and normal brain (primarily localized to astrocytes). The signal intensity in the glioblastomas appeared to be greater than that in normal astrocytes. While the majority of glioma and glioblastoma samples tested were positive for TAT152 expression, the majority of normal brain samples tested were negative for such expression.

(40) DNA167234 (TAT130)

Seventy cases of primary adenocarcinoma of the prostate were available for review. Of these 70 cases, 56 cases (80%) are positive for TAT130 expression. TAT130 expression in non-prostatic tissues is weak or undetectable.

(41) DNA235621 (TAT166)

Seventy cases of primary adenocarcinoma of the prostate were available for review. Of these 70 cases, 56 cases (80%) are positive for TAT166 expression. TAT166 expression in non-prostatic tissues is weak or undetectable.

(42) DNA236493 (TAT141)

Positive expression is observed in 70/148 breast carcinomas, 2/63 colorectal adenocarcinomas, 4/42 ovarian tumors, 9/69 non small cell lung carcinomas, 9/67 prostate adenocarcinomas and 5/23 gliomas. Expression in normal non-cancerous tissues appears restricted to prostate and breast epithelium.

(43) DNA226094 (TAT164)

Twenty one of 37 glioblastoma samples and 8 of 8 glioma samples were positive for TAT164 expression while all other tumor and normal tissues examined (including normal brain tissue) were negative.

(44) DNA227578 (TAT165)

Fifteen of 25 glioblastoma samples tested were positive for expression while significantly weaker expression was observed in the normal brain samples tested.

EXAMPLE 5: Immunohistochemistry Analysis

Antibodies against certain TAT polypeptides disclosed herein were prepared and immunohistochemistry analysis was performed as follows. Tissue sections were first fixed for 5 minutes in acetone/ethanol (frozen or paraffin-embedded). The sections were then washed in PBS and then blocked with avidin and biotin (Vector kit) for 10 minutes each followed by a wash in PBS. The sections were then blocked with 10% serum for 20 minutes and then blotted to remove the excess. A primary antibody was then added to the sections at a concentration of 10 μ g/ml for 1 hour and then the sections were washed in PBS. A biotinylated secondary antibody (anti-primary antibody) was then added to the sections for 30 minutes and then the sections were washed with PBS. The sections were then exposed to the reagents of the Vector ABC kit for 30 minutes and then the sections were washed in PBS. The sections were then exposed to Diaminobenzidine (Pierce) for 5 minutes and then washed in PBS. The sections were then counterstained with Mayers hematoxylin, covered with a coverslip and visualized. Immunohistochemistry analysis can also be performed as described in Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989 and Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). The results from these analyses are show below.

(1) DNA96930 (TAT112)

Significantly higher expression was detected in the apical surface of the colonic crypts of colon tumors than on the apical surface of the normal colonic crypts. Additionally, TAT112 was found to be significantly overexpressed in pancreatic adenocarcinoma cells as compared to normal pancreatic cells. Finally, IHC analysis performed as described above evidenced that TAT112 is significantly overexpressed in lung carcinoma as compared to normal lung tissue, non small cell lung carcinoma as compared to normal lung tissue and stomach carcinoma as compared to normal stomach tissue.

(2) DNA226539 (TAT126)

Positive expression is observed in 2/10 uterine adenocarcinomas, 9/17 ovarian adenocarcinomas and 2/20 non small cell lung carcinomas. Using this procedure, expression of TAT126 was not detectable in any normal tissue.

(3) DNA236511 (TAT151)

Positive expression is observed in 2/10 uterine adenocarcinomas, 9/17 ovarian adenocarcinomas and 2/20 non small cell lung carcinomas. Using this procedure, expression of TAT151 was not detectable in any normal tissue.

EXAMPLE 6: Verification and Analysis of Differential TAT Polypeptide Expression by GEPIS

TAT polypeptides which may have been identified as a tumor antigen as described in one or more of the above Examples were analyzed and verified as follows. An expressed sequence tag (EST) DNA database (LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) was searched and interesting EST sequences were identified by GEPIS. Gene expression profiling *in silico* (GEPIS) is a bioinformatics tool developed at Genentech, Inc. that characterizes genes of interest for new cancer therapeutic targets. GEPIS takes advantage of large amounts of EST sequence and library information to determine gene expression profiles. GEPIS is

capable of determining the expression profile of a gene based upon its proportional correlation with the number of its occurrences in EST databases, and it works by integrating the LIFESEQ® EST relational database and Genentech proprietary information in a stringent and statistically meaningful way. In this example, GEPIS is used to identify and cross-validate novel tumor antigens, although GEPIS can be configured to perform either very specific analyses or broad screening tasks. For the initial screen, GEPIS is used to identify EST sequences from the LIFESEQ® database that correlate to expression in a particular tissue or tissues of interest (often a tumor tissue of interest). The EST sequences identified in this initial screen (or consensus sequences obtained from aligning multiple related and overlapping EST sequences obtained from the initial screen) were then subjected to a screen intended to identify the presence of at least one transmembrane domain in the encoded protein. Finally, GEPIS was employed to generate a complete tissue expression profile for the various sequences of interest. Using this type of screening bioinformatics, various TAT polypeptides (and their encoding nucleic acid molecules) were identified as being significantly overexpressed in a particular type of cancer or certain cancers as compared to other cancers and/or normal non-cancerous tissues. The rating of GEPIS hits is based upon several criteria including, for example, tissue specificity, tumor specificity and expression level in normal essential and/or normal proliferating tissues. The following is a list of molecules whose tissue expression profile as determined by GEPIS evidences high tissue expression and significant upregulation of expression in a specific tumor or tumors as compared to other tumor(s) and/or normal tissues and optionally relatively low expression in normal essential and/or normal proliferating tissues. As such, the molecules listed below are excellent polypeptide targets for the diagnosis and therapy of cancer in mammals.

	<u>Molecule</u>	<u>upregulation of expression in:</u>	<u>as compared to:</u>
20	DNA77507 (TAT161)	breast tumor	normal breast tissue
	DNA77507 (TAT161)	colon tumor	normal colon tissue
	DNA77507 (TAT161)	lung tumor	normal lung tissue
	DNA77507 (TAT161)	kidney tumor	normal kidney tissue
	DNA77507 (TAT161)	liver tumor	normal liver tissue
25	DNA77507 (TAT161)	ovarian tumor	normal ovarian tissue
	DNA77507 (TAT161)	pancreatic tumor	normal pancreatic tissue
	DNA77507 (TAT161)	rectum tumor	normal rectum tissue
	DNA77507 (TAT161)	skin tumor	normal skin tissue
	DNA77507 (TAT161)	uterine tumor	normal uterine tissue
30	DNA77507 (TAT161)	brain tumor	normal brain tissue
	DNA77507 (TAT161)	soft tissue tumor	normal soft tissue
	DNA77507 (TAT161)	bone tumor	normal bone tissue
	DNA82343 (TAT157)	colon tumor	normal colon tissue
	DNA82343 (TAT157)	ovarian tumor	normal ovarian tissue
35	DNA82343 (TAT157)	stomach tumor	normal stomach tissue
	DNA82343 (TAT157)	thymus tumor	normal thymus tissue
	DNA82343 (TAT157)	small intestine tumor	normal small intestine tissue
	DNA87994 (TAT160)	breast tumor	normal breast tissue
	DNA87994 (TAT160)	pancreatic tumor	normal pancreatic tissue
40	DNA87994 (TAT160)	colon tumor	normal colon tissue
	DNA87994 (TAT160)	esophagus tumor	normal esophagus tissue
	DNA87994 (TAT160)	ovarian tumor	normal ovarian tissue
	DNA87994 (TAT160)	prostate tumor	normal prostate tissue
	DNA88131 (TAT158)	breast tumor	normal breast tissue
45	DNA88131 (TAT158)	colon tumor	normal colon tissue
	DNA88131 (TAT158)	lung tumor	normal lung tissue

	Molecule	upregulation of expression in:	as compared to:
	DNA88131 (TAT158)	pancreatic tumor	normal pancreatic tissue
	DNA88131 (TAT158)	prostate tumor	normal prostate tissue
	DNA88131 (TAT158)	stomach tumor	normal stomach tissue
	DNA88131 (TAT158)	bladder tumor	normal bladder tissue
5	DNA88131 (TAT158)	brain tumor	normal brain tissue
	DNA95930 (TAT110)	colon tumor	normal colon tissue
	DNA95930 (TAT110)	lung tumor	normal lung tissue
	DNA95930 (TAT110)	prostate tumor	normal prostate tissue
	DNA95930 (TAT110)	endometrial tumor	normal endometrial tissue
10	DNA95930 (TAT110)	ovarian tumor	normal ovarian tissue
	DNA95930 (TAT110)	breast tumor	normal breast tissue
	DNA95930-1 (TAT210)	colon tumor	normal colon tissue
	DNA95930-1 (TAT210)	lung tumor	normal lung tissue
	DNA95930-1 (TAT210)	prostate tumor	normal prostate tissue
15	DNA95930-1 (TAT210)	endometrial tumor	normal endometrial tissue
	DNA95930-1 (TAT210)	ovarian tumor	normal ovarian tissue
	DNA95930-1 (TAT210)	breast tumor	normal breast tissue
	DNA96917 (TAT159)	pancreatic tumor	normal pancreatic tissue
	DNA96917 (TAT159)	lung tumor	normal lung tissue
20	DNA96917 (TAT159)	liver tumor	normal liver tissue
	DNA96917 (TAT159)	prostate tumor	normal prostate tissue
	DNA96930 (TAT112)	breast tumor	normal breast tissue
	DNA96930 (TAT112)	colon tumor	normal colon tissue
	DNA96930 (TAT112)	lung tumor	normal lung tissue
25	DNA96930 (TAT112)	ovarian tumor	normal ovarian tissue
	DNA96930 (TAT112)	pancreatic tumor	normal pancreatic tissue
	DNA96930 (TAT112)	stomach tumor	normal stomach tissue
	DNA96936 (TAT147)	breast tumor	normal breast tissue
	DNA96936 (TAT147)	colon tumor	normal colon tissue
30	DNA96936 (TAT147)	prostate tumor	normal prostate tissue
	DNA96936 (TAT147)	uterine tumor	normal uterine tissue
	DNA98565 (TAT145)	brain tumor	normal brain tissue
	DNA98565 (TAT145)	colon tumor	normal colon tissue
	DNA246435 (TAT152)	brain tumor	normal brain tissue
35	DNA246435 (TAT152)	colon tumor	normal colon tissue
	DNA98591 (TAT162)	colon tumor	normal colon tissue
	DNA98591 (TAT162)	small intestine tumor	normal small intestine tissue
	DNA98591 (TAT162)	ovarian tumor	normal ovarian tissue
	DNA98591 (TAT162)	esophagus tumor	normal esophagus tissue
40	DNA108809 (TAT114)	colon tumor	normal colon tissue
	DNA108809 (TAT114)	lung tumor	normal lung tissue
	DNA108809 (TAT114)	ovarian tumor	normal ovarian tissue
	DNA108809 (TAT114)	brain tumor	normal brain tissue
	DNA143493 (TAT103)	breast tumor	normal breast tissue
45	DNA167234 (TAT130)	prostate tumor	normal prostate tissue
	DNA235621 (TAT160)	prostate tumor	normal prostate tissue
	DNA176766 (TAT132)	kidney tumor	normal kidney tissue
	DNA176766 (TAT132)	uterine tumor	normal uterine tissue
	DNA236463 (TAT150)	kidney tumor	normal kidney tissue
50	DNA236463 (TAT150)	uterine tumor	normal uterine tissue
	DNA181162 (TAT129)	prostate tumor	normal prostate tissue
	DNA188221 (TAT111)	colon tumor	normal colon tissue
	DNA188221 (TAT111)	liver tumor	normal liver tissue
	DNA188221 (TAT111)	lung tumor	normal lung tissue
55	DNA233876 (TAT146)	colon tumor	normal colon tissue

	<u>Molecule</u>	<u>upregulation of expression in:</u>	<u>as compared to:</u>
	DNA233876 (TAT146)	liver tumor	normal liver tissue
	DNA233876 (TAT146)	lung tumor	normal lung tissue
	DNA193891 (TAT148)	prostate tumor	normal prostate tissue
	DNA193891 (TAT148)	breast tumor	normal breast tissue
5	DNA248170 (TAT187)	breast tumor	normal breast tissue
	DNA248170 (TAT187)	prostate tumor	normal prostate tissue
	DNA194628 (TAT118)	kidney tumor	normal kidney tissue
	DNA246415 (TAT167)	kidney tumor	normal kidney tissue
	DNA215609 (TAT113)	colon tumor	normal colon tissue
10	DNA220432 (TAT128)	prostate tumor	normal prostate tissue
	DNA226094 (TAT164)	breast tumor	normal breast tissue
	DNA226094 (TAT164)	brain tumor	normal brain tissue
	DNA226094 (TAT164)	ovarian tumor	normal ovarian tissue
	DNA226094 (TAT164)	lung tumor	normal lung tissue
15	DNA226165 (TAT122)	breast tumor	normal breast tissue
	DNA226165 (TAT122)	endometrial tumor	normal endometrial tissue
	DNA226165 (TAT122)	lung tumor	normal lung tissue
	DNA226165 (TAT122)	colon tumor	normal colon tissue
	DNA226237 (TAT117)	kidney tumor	normal kidney tissue
20	DNA246450 (TAT168)	kidney tumor	normal kidney tissue
	DNA246450 (TAT168)	brain tumor	normal brain tissue
	DNA226456 (TAT144)	breast tumor	normal breast tissue
	DNA226456 (TAT144)	brain tumor	normal brain tissue
	DNA226456 (TAT144)	endometrial tumor	normal endometrial tissue
25	DNA226456 (TAT144)	kidney tumor	normal kidney tissue
	DNA226456 (TAT144)	lung tumor	normal lung tissue
	DNA237637 (TAT188)	breast tumor	normal breast tissue
	DNA237637 (TAT188)	brain tumor	normal brain tissue
	DNA237637 (TAT188)	endometrial tumor	normal endometrial tissue
30	DNA237637 (TAT188)	kidney tumor	normal kidney tissue
	DNA237637 (TAT188)	lung tumor	normal lung tissue
	DNA226539 (TAT126)	colon tumor	normal colon tissue
	DNA226539 (TAT126)	endometrial tumor	normal endometrial tissue
	DNA226539 (TAT126)	ovarian tumor	normal ovarian tissue
35	DNA226539 (TAT126)	pancreatic tumor	normal pancreatic tissue
	DNA236511 (TAT151)	colon tumor	normal colon tissue
	DNA236511 (TAT151)	endometrial tumor	normal endometrial tissue
	DNA236511 (TAT151)	ovarian tumor	normal ovarian tissue
	DNA236511 (TAT151)	pancreatic tumor	normal pancreatic tissue
40	DNA226771 (TAT115)	colon tumor	normal colon tissue
	DNA227087 (TAT163)	breast tumor	normal breast tissue
	DNA227087 (TAT163)	colon tumor	normal colon tissue
	DNA227087 (TAT163)	endocrine tumor	normal endocrine tissue
	DNA227087 (TAT163)	kidney tumor	normal kidney tissue
45	DNA227087 (TAT163)	liver tumor	normal liver tissue
	DNA227087 (TAT163)	lung tumor	normal lung tissue
	DNA227087 (TAT163)	pancreatic tumor	normal pancreatic tissue
	DNA227087 (TAT163)	uterine tumor	normal uterine tissue
	DNA227087 (TAT163)	prostate tumor	normal prostate tissue
50	DNA227087 (TAT163)	bladder tumor	normal bladder tissue
	DNA266307 (TAT227)	breast tumor	normal breast tissue
	DNA266307 (TAT227)	colon tumor	normal colon tissue
	DNA266307 (TAT227)	endocrine tumor	normal endocrine tissue
	DNA266307 (TAT227)	kidney tumor	normal kidney tissue
55	DNA266307 (TAT227)	liver tumor	normal liver tissue

	<u>Molecule</u>	<u>upregulation of expression in:</u>	<u>as compared to:</u>
5	DNA266307 (TAT227)	lung tumor	normal lung tissue
	DNA266307 (TAT227)	pancreatic tumor	normal pancreatic tissue
	DNA266307 (TAT227)	uterine tumor	normal uterine tissue
	DNA266307 (TAT227)	prostate tumor	normal prostate tissue
	DNA266307 (TAT227)	bladder tumor	normal bladder tissue
10	DNA266311 (TAT228)	breast tumor	normal breast tissue
	DNA266311 (TAT228)	colon tumor	normal colon tissue
	DNA266311 (TAT228)	endocrine tumor	normal endocrine tissue
	DNA266311 (TAT228)	kidney tumor	normal kidney tissue
	DNA266311 (TAT228)	liver tumor	normal liver tissue
15	DNA266311 (TAT228)	lung tumor	normal lung tissue
	DNA266311 (TAT228)	pancreatic tumor	normal pancreatic tissue
	DNA266311 (TAT228)	uterine tumor	normal uterine tissue
	DNA266311 (TAT228)	prostate tumor	normal prostate tissue
	DNA266311 (TAT228)	bladder tumor	normal bladder tissue
20	DNA266312 (TAT229)	breast tumor	normal breast tissue
	DNA266312 (TAT229)	colon tumor	normal colon tissue
	DNA266312 (TAT229)	endocrine tumor	normal endocrine tissue
	DNA266312 (TAT229)	kidney tumor	normal kidney tissue
	DNA266312 (TAT229)	liver tumor	normal liver tissue
25	DNA266312 (TAT229)	lung tumor	normal lung tissue
	DNA266312 (TAT229)	pancreatic tumor	normal pancreatic tissue
	DNA266312 (TAT229)	uterine tumor	normal uterine tissue
	DNA266312 (TAT229)	prostate tumor	normal prostate tissue
	DNA266312 (TAT229)	bladder tumor	normal bladder tissue
30	DNA266313 (TAT230)	breast tumor	normal breast tissue
	DNA266313 (TAT230)	colon tumor	normal colon tissue
	DNA266313 (TAT230)	endocrine tumor	normal endocrine tissue
	DNA266313 (TAT230)	kidney tumor	normal kidney tissue
	DNA266313 (TAT230)	liver tumor	normal liver tissue
35	DNA266313 (TAT230)	lung tumor	normal lung tissue
	DNA266313 (TAT230)	pancreatic tumor	normal pancreatic tissue
	DNA266313 (TAT230)	uterine tumor	normal uterine tissue
	DNA266313 (TAT230)	prostate tumor	normal prostate tissue
	DNA266313 (TAT230)	bladder tumor	normal bladder tissue
40	DNA227224 (TAT121)	breast tumor	normal breast tissue
	DNA227224 (TAT121)	endometrial tumor	normal endometrial tissue
	DNA227224 (TAT121)	lung tumor	normal lung tissue
	DNA227224 (TAT121)	skin tumor	normal skin tissue
	DNA247486 (TAT183)	breast tumor	normal breast tissue
45	DNA247486 (TAT183)	endometrial tumor	normal endometrial tissue
	DNA247486 (TAT183)	lung tumor	normal lung tissue
	DNA247486 (TAT183)	skin tumor	normal skin tissue
	DNA227578 (TAT165)	brain tumor	normal brain tissue
	DNA227800 (TAT131)	prostate tumor	normal prostate tissue
50	DNA227800 (TAT131)	kidney tumor	normal kidney tissue
	DNA227904 (TAT140)	breast tumor	normal breast tissue
	DNA228199 (TAT127)	uterine tumor	normal uterine tissue
	DNA228199 (TAT127)	fallopian tube tumor	normal fallopian tube tissue
	DNA228199 (TAT127)	ovarian tumor	normal ovarian tissue
55	DNA228199 (TAT127)	lung tumor	normal lung tissue
	DNA228201 (TAT116)	colon tumor	normal colon tissue
	DNA247488 (TAT189)	colon tumor	normal colon tissue
	DNA236538 (TAT190)	colon tumor	normal colon tissue
	DNA247489 (TAT191)	colon tumor	normal colon tissue

	Molecule	upregulation of expression in:	as compared to:
	DNA231312 (TAT143)	colon tumor	normal colon tissue
	DNA231542 (TAT100)	brain tumor	normal brain tissue
	DNA231542 (TAT100)	glioma	normal glial tissue
5	DNA231542-1 (TAT284)	brain tumor	normal brain tissue
	DNA231542-1 (TAT284)	glioma	normal glial tissue
	DNA231542-2 (TAT285)	brain tumor	normal brain tissue
	DNA231542-2 (TAT285)	glioma	normal glial tissue
	DNA297393 (TAT285-1)	brain tumor	normal brain tissue
	DNA297393 (TAT285-1)	glioma	normal glial tissue
10	DNA232754 (TAT125)	lung tumor	normal lung tissue
	DNA236246 (TAT153)	breast tumor	normal breast tissue
	DNA236343 (TAT104)	breast tumor	normal breast tissue
	DNA236493 (TAT141)	breast tumor	normal breast tissue
	DNA236493 (TAT141)	glioblastoma tumor	normal glial tissue
15	DNA236534 (TAT102)	breast tumor	normal breast tissue
	DNA236534 (TAT102)	lung tumor	normal lung tissue
	DNA236534 (TAT102)	pancreatic tumor	normal pancreatic tissue
	DNA236534 (TAT102)	prostate tumor	normal prostate tissue
	DNA236534 (TAT102)	bladder tumor	normal bladder tissue
20	DNA247480 (TAT142)	lung tumor	normal lung tissue
	DNA264454 (TAT106)	breast tumor	normal breast tissue
	DNA264454 (TAT106)	prostate tumor	normal prostate tissue
	DNA264454 (TAT106)	ovarian tumor	normal ovarian tissue

25 EXAMPLE 7: Use of TAT as a hybridization probe

The following method describes use of a nucleotide sequence encoding TAT as a hybridization probe for, i.e., diagnosis of the presence of a tumor in a mammal.

30 DNA comprising the coding sequence of full-length or mature TAT as disclosed herein can also be employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of TAT) in human tissue cDNA libraries or human tissue genomic libraries.

35 Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled TAT-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence TAT can then be identified using standard techniques known in the art.

EXAMPLE 8: Expression of TAT in *E. coli*

40 This example illustrates preparation of an unglycosylated form of TAT by recombinant expression in *E. coli*.

The DNA sequence encoding TAT is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and

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tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STH codons, polyhis sequence, and enterokinase cleavage site), the TAT coding region, lambda transcriptional terminator, and an argU gene.

5 The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

10 Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized TAT protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

15 TAT may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding TAT is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(hipRts) clpP(jacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g
20 Difco yeast extract, 5.36 g Sheffield lyecase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55 % (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

30 *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate
35 column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Ultrapure grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the

desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded TAT polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using Q25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 9: Expression of TAT in mammalian cells

This example illustrates preparation of a potentially glycosylated form of TAT by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the TAT DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the TAT DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-TAT.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-TAT DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thinnappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The

293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μ Cl/ml 35 S-cysteine and 200 μ Cl/ml 35 S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of TAT polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, TAT may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-TAT DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed TAT can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, TAT can be expressed in CHO cells. The pRK5-TAT can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as 35 S-methionine. After determining the presence of TAT polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed TAT can then be concentrated and purified by any selected method.

Epitope-tagged TAT may also be expressed in host CHO cells. The TAT may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged TAT insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged TAT can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

TAT may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuffling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect[®] (Qiagen), Dospert[®] or Eugene[®] (Boehringer Mannheim). The cells are grown as described in Lucas et al., *supra*. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μ m filtered PS20 with 5% 0.2 μ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μ m filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting

1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 10: Expression of TAT in Yeast

The following method describes recombinant expression of TAT in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of TAT from the ADH2/GAPDH promoter. DNA encoding TAT and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of TAT. For secretion, DNA encoding TAT can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native TAT signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of TAT.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant TAT can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing TAT may further be purified using selected column chromatography resins.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 11: Expression of TAT in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of TAT in Baculovirus-infected insect cells.

The sequence coding for TAT is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding TAT or the desired portion of the coding sequence of TAT such as the sequence encoding an extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGoldTM virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilly

et al., Raculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged TAT can then be purified, for example, by Ni^{2+} -chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl_2 ; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+} -NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni^{2+} -NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₆-tagged TAT are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fe tagged) TAT can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Certain of the TAT polypeptides disclosed herein have been successfully expressed and purified using this technique(s).

EXAMPLE 12: Preparation of Antibodies that Bind TAT

This example illustrates preparation of monoclonal antibodies which can specifically bind TAT.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified TAT, fusion proteins containing TAT, and cells expressing recombinant TAT on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the TAT immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-TAT antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of TAT. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells

which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against TAT. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against TAT is within the skill in the art.

5 The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-TAT monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

10 Antibodies directed against certain of the TAT polypeptides disclosed herein have been successfully produced using this technique(s). More specifically, functional monoclonal antibodies that are capable of recognizing and binding to TAT protein (as measured by standard ELISA, FACS sorting analysis and/or immunohistochemistry analysis) have been successfully generated against the following TAT proteins as disclosed herein: TAT110 (DNA95930), TAT210 (DNA95930-1), TAT113 (DNA215609), TAT126 (DNA226539), TAT151 (DNA236511), TAT111 (DNA188221), TAT146 (DNA233876), TAT112 (DNA96930), TAT145 (DNA98565), TAT152 (DNA246435), TAT141 (DNA236493), TAT114 (DNA108809), TAT104 (DNA236343), TAT100 (DNA231542), TAT284 (DNA231542-1), TAT285 (DNA231542-2), TAT285-1 (DNA297393), TAT144 (DNA226456), TAT188 (DNA237637), TAT123 (DNA210499), TAT211 (DNA219894), TAT102 (DNA236534), TAT127 (DNA228199) and TAT128 (DNA220432). Interestingly, Applicants have identified that the monoclonal antibodies prepared against TAT111 (DNA188221) and TAT146 (DNA233876) are capable of blocking activation of the EphB2R receptor encoded by the DNA188221 and DNA233876 molecules by its associated ligand polypeptide. As such, antibodies and methods for using those antibodies for blocking activation of the EphB2R receptor (i.e., TAT111 and TAT146 polypeptides) by its associated ligand are encompassed within the presently described invention. Moreover, Applicants have identified that monoclonal antibodies directed against the TAT110 (DNA95930) and TAT210 (DNA95930-1) polypeptides (i.e., IL-20 receptor alpha polypeptides) are capable of inhibiting activation of the IL20 receptor alpha by IL-19 protein. As such, antibodies and methods for using those antibodies for inhibiting activation of the IL-20 receptor alpha (i.e., TAT110 and TAT210 polypeptides) by IL-19 are encompassed within the presently described invention.

30 In addition to the successful preparation of monoclonal antibodies directed against the TAT polypeptides as described herein, many of those monoclonal antibodies have been successfully conjugated to a cell toxin for use in directing the cellular toxin to a cell (or tissue) that expresses a TAT polypeptide of interest (both *in vitro* and *in vivo*). For example, toxin (e.g., DM1) derivitized monoclonal antibodies have been successfully generated to the following TAT polypeptides as described herein: TAT110 (DNA95930), TAT210 (DNA95930-1), TAT112 (DNA96930), TAT113 (DNA215609), TAT111 (DNA188221) and TAT146 (DNA233876).

EXAMPLE 13: Purification of TAT Polypeptides Using Specific Antibodies

Native or recombinant TAT polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-TAT polypeptide, mature TAT polypeptide, or pre-TAT polypeptide is purified by immunoaffinity chromatography using antibodies specific for the TAT polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-TAT polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of TAT polypeptide by preparing a fraction from cells containing TAT polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble TAT polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble TAT polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TAT polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/TAT polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and TAT polypeptide is collected.

EXAMPLE 14: *In Vitro* Tumor Cell Killing Assay

Mammalian cells expressing the TAT polypeptide of interest may be obtained using standard expression vector and cloning techniques. Alternatively, many tumor cell lines expressing TAT polypeptides of interest are publicly available, for example, through the ATCC and can be routinely identified using standard ELISA or FACS analysis. Anti-TAT polypeptide monoclonal antibodies (and toxin conjugated derivatives thereof) may then be employed in assays to determine the ability of the antibody to kill TAT polypeptide expressing cells *in vitro*.

For example, cells expressing the TAT polypeptide of interest are obtained as described above and plated into 96 well dishes. In one analysis, the antibody/toxin conjugate (or naked antibody) is included throughout the cell incubation for a period of 4 days. In a second independent analysis, the cells are incubated for 1 hour with the antibody/toxin conjugate (or naked antibody) and then washed and incubated in the absence of antibody/toxin conjugate for a period of 4 days. Cell viability is then measured using the CellTiter-Glo Luminescent Cell Viability Assay from Promega (Cat# G7571). Untreated cells serve as a negative control.

In one specific analysis, the ability of monoclonal antibodies directed against TAT112 (DNA96930) were analyzed for the ability to kill cells expressing that polypeptide. In one analysis, an expression vector called gD.NCA was prepared. The TAT112 polypeptide encoding sequences inserted into that vector are driven by an SV40 promoter and the vector also contains the SV40 early poly A signal. The gD.NCA vector was co-transfected into PC3 cells along with an SV40 vector that expresses Neo resistance in PC3 cells, and positive transformants were selected in 800 μ g/ml G418. Positive clones were isolated in 96 well plates and analyzed by flow cytometry using an anti-TAT112 monoclonal antibody prepared as described above and called 3E6. Clone 3 was selected for the analysis as it was found to express a high level of TAT112 polypeptide on its surface. In a second independent analysis, the pancreatic cancer cell line, Hpa1 II, was obtained from the ATCC and employed in the assay.

The results from the above described assay demonstrated that DM1-conjugated anti-TAT112 monoclonal antibodies were highly efficacious in killing both the TAT112 expressing PC3 cell line as well as the pancreatic cancer cell line Hpa1 II as compared to the untreated negative controls.

EXAMPLE 15: *In Vivo* Tumor Cell Killing Assay

To test the efficacy of unconjugated anti-TAT112 monoclonal antibodies, anti-TAT112 antibody was injected intraperitoneally into nude mice 24 hours prior to receiving PC3.gD.NCA clone 3 cells (obtained as described in Example 14 above) subcutaneously in the flank. Antibody injections continued twice per week for the remainder of the study. Tumor volume was measured twice per week.

To test the efficacy of DM1-conjugated anti-TAT112 antibody, PC3.gD.NCA clone 3 cells (obtained as described in Example 14 above) were inoculated into the flank of nude mice. When the tumors reached a mean volume of approximately 100mm³, mice were treated with DM1-conjugated anti-TAT112 antibody intravenously either once or twice per week.

The results of the above analyses demonstrated that both the unconjugated anti-TAT112 as well as the DM1-conjugated anti-TAT112 antibody were highly efficacious in reducing tumor volume in this *in vivo* model. These analyses demonstrate that anti-TAT polypeptide monoclonal antibodies are efficacious for killing tumor cells that express a TAT polypeptide of interest.

EXAMPLE 16: Northern Blot Analysis

Northern blot analysis was performed essentially as described by Sambrook et al., *supra*. Northern blot analysis using probes derived from DNA231542, DNA231542-1, DNA231542-2 and DNA297393 evidences significant upregulation of expression in human glioma tissue as compared to normal human brain tissue.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any

aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. An isolated antibody that binds to a polypeptide having at least 80% amino acid sequence identity to:
 - (a) the polypeptide shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154);
 - (b) the polypeptide shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154), lacking its associated signal peptide;
 - (c) an extracellular domain of the polypeptide shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154), with its associated signal peptide;
 - (d) an extracellular domain of the polypeptide shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154), lacking its associated signal peptide;
 - (e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1 to 78A-B (SEQ ID NOS:1-78); or
 - (f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1 to 78A-B (SEQ ID NOS:1-78).
2. An isolated antibody that binds to a polypeptide having:
 - (a) the amino acid sequence shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154);
 - (b) the amino acid sequence shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154), lacking its associated signal peptide sequence;
 - (c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154), with its associated signal peptide sequence;
 - (d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 79 to 154 (SEQ ID NOS:79-154), lacking its associated signal peptide sequence;
 - (e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1 to 78A-B (SEQ ID NOS:1-78); or
 - (f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1 to 78A-B (SEQ ID NOS:1-78).
3. The antibody of Claim 1 which is a monoclonal antibody.
4. The antibody of Claim 1 which is an antibody fragment.
5. The antibody of Claim 1 which is a chimeric or a humanized antibody.
6. The antibody of Claim 1 which is conjugated to a growth inhibitory agent.
7. The antibody of Claim 1 which is conjugated to a cytotoxic agent.

8. The antibody of Claim 7, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.
9. The antibody of Claim 7, wherein the cytotoxic agent is a toxin.
- 5 10. The antibody of Claim 9, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.
11. The antibody of Claim 9, wherein the toxin is a maytansinoid.
- 10 12. The antibody of Claim 1 which is produced in bacteria.
13. The antibody of Claim 1 which is produced in CHO cells.
14. The antibody of Claim 1 which induces death of a cell to which it binds.
- 15 15. The antibody of Claim 1 which is detectably labeled.

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FIGURE 1

CCAGAATTCCGSCACGAGGGTGRCCCGGACAGCTGTCTCTCTGACACCACCCCGGCCTGCCTCTTTGTTGCCA
TGAGAGCTGCCTACCTCTTCTGCTATTCCCTGCCGTCAGGCTTGCTGGCTCAGGGCCAGTATGACCTGGACCCG
CTGCCGCCGTTCCCTGACCACGTCCAGTACACCCACTATAGCGACCAGATCGACAACCCAGACTACTATGATTA
TCAGSAGGTGACTCCTCGGCCCTCCGAGGAACASTTCCAGTTCCAGTCCCAGCAGCAAGTCCAACAGGAAGTCA
TCCCAGCCCCAACCCAGAACAGGAATGCAGAGCTGGAGCCCCACAGAGCCTGGGCCCTCTTGACTGCCGTGAG
GAACAGTACCCGTGCACCCGCCCTCTACTCCATACACAGGCCCTTGCAAACAGTGTCTCAACGAGGTCTGCTTCTA
CAGCCTCCGCCCTGTGTACGTCAATTAACAAGGAGATCTGTGTTCCGTACAGTGTGTGCCACGAGGAGCTCCTCC
GAGCTGACCTCTGTGCGGACAAAGTTCTCCAAATGTGGCGTGATGGCCAGCAGCGGCCCTGTGCCAATCCGTGGCG
GCCTCCTGTGCCAGGAGCTGTGGGAGCTGCTAGGCTGGTGGCTGGCATCCTGAGTCCCTGGCCCTCCTGGGATCTG
GGGCCCTCGGGCCCTGCCTGACCTGGTGCTTTTTTCCCCATCCCCATGTTCCCTTTTATTCGTAAAAAGTTAGT
GCACTGCAGCCCTGGGGGTTGCAGGCTGCGGTGCCCTCAGGGCCCCCTCCTTCAGCCTGTGGCCACCTCTGGGGCAC
GATGGGGGCTCCCCACTGCCAGTCTGCCCTCGGGTTGGGGGAGTATCCCAGGCCCTCTCTGTGGGACCTGGGC
CCCTGACGCGCCTTCTCAGCCCGTTTTCAGGACAGACAGTCCCCCGAGGTAGGCTACATCCCCCACCCAGCT
GGTCTGCTTGGATTCCTACAGCCCCCTGGGCATGGACCACTTTAFTTTATACAAATTAAAAACAAGTTTTAC

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FIGURE 2A

CACTAACGCTCTTCCTAGTCCCGGGCCAACTCGGACAGTFTTGCTCATTATTGCAACGGTCAAGGCTGGCTTG
 TSCCAGAACGGCGCGCGCGCGACGACGACACACACGSSGGGAAACTTTTTTAAAAATGAAAGGCTAGAAAGG
 CTCAGCGGGCGGGCGGGGCCGTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCGAGGAATCCCTCCGGTCCGGA
 CGCCCCGGCCCCGCTCGGCGCCCCGCTGGGATGGTGCAGCGCTCGCCCGGGGGCCGAGAGCTGCTGCACTGAAG
 GCGGGCGACGATGGCAGCGCGGCGGCTGCCCCGTGTCCCCCGCCCCCGCCCTCCTGCTCGCCCTGCGCGGTGCTC
 TGCTCGCGCCCTGCGAGGCCCCGAGGGGTGAGCTTATGGAACGAAGGAAGAGCTGATGAAGTTGTCAGTGCCTCT
 GTTCGAGTGGGACCTCTGGATCCGAGTGAAGAGCTTCGACTCCAAGATCATCCAGAAGTGTGAATATTGG
 ACTACAAACGGGAAAGCAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGG
 AAACCCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGTAATTCGCGTCACTGTTAC
 TACCATGGACBTGTACGGGATATTCTGATTTCAGCAGTCACTCTCAGCACGTGTTCTGGTCTCAGGGGACTTAT
 TGTGTTTGAAGATGAAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACCTTCCAGCGA
 AGAAGCTGAAGAGCGTCCGGGGATCATGTGGATCACATCACACACACCAACCTCGCTGCAAGAAATGTGTTT
 CCACCAACCTCTCAGACATGGGCAAGAAAGCATAAAGAGAGACCCCTCAAGGCAACTAAGTATGTGGAGCTGGT
 GATCGTGGCAGACAAACGAGAGTTTCAGAGGCAAGGAAAAGATCTGGAAGAAATTAAGCAGCGATTAAAGAGA
 TTGCTAATCACGTTGACAAGTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAAGTGTGGAAT
 GACATGGACAAATGCTCTGTAAAGTCAGGACCCATTACACAGCCTTCATGAATTTCTGGACTGGAGCAAGATGAA
 GCTTCTACCTCGCAATCCCATGACAATGCGCAGCTTGTGAGTGGGTTTATTTCCAAGGGACCAACATCGGCA
 TGGCCCCAATCATGAGCATGTGCACGGCAGACCACTGTGGGGAAATTTCTATGGACCAATCAGACAATCCCTTT
 GGTGCAAGCGTGAACCTGGCAGATGAGCTGGGGCACAAATTTGGGATGAATCATGACACACTGGACAGGGGCTG
 TAGCTGTCAAATGGCGGTTGAGAAAGGAGGCTGCATCATGAAGCCTTCCACCGGGTACCCATTTCCCATGGTGT
 TCAGCAGTTCAGCAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACCTGCCG
 GAAGTCAGGGAGTCTTTCCGGGGCCAGAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGG
 CGAGCCAGAGGAATGTATGAATTCCTGCTGCAATGCCACCACTGTACCTGAAGCCGGACGCTGTGTGCGCAC
 ATGGGCTGTGCTGTGAAGACTGCCAGCTGAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGAC
 CTCCAGAGTTCTGCACAGGGGCCAGCCCTCACTGCCAGCCAACGTGTACCTGCACGATGGGCACTCATGTCA
 GGATGTGGACGGCTACTGTACAAATGGCATCTGCCAGACTCACGAGCAGCAGTGTGTACACTCTGGGGACCAG
 GTGCTAAACCTGCCCCGGAATCTGCTTTGAGAGAGTCAATTTCTGCAGGTGATCCTTATGGCAACTGTGGCAAA
 GTCTCGAAGAGTTCCTTTGCCAAATGCGAGATGAGAGATGCTAAATGTGGABAAATCCAGTGTCAAGGAGGTGC
 CAGCCGGCCAGTCATTGGTACCAATGCCGTTTCCATAGAAACAAACATCCCCCTGCAGCAAGGAGGCCCCGATT
 TGTGCCCCGGGGACCCACGTGTACTTGGGCGATGACATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGT
 GCAGATGGAAAATCTGCTGAATCGTCAATGTCAAAATATTAGTGTCTTTGGGTTACAGAGTGTGCAATGCA
 GTSCCAGGAGAGGGGTGTGCAACACAGGAAGAACTGCCACTGCGAGGCCCCACTGGGCACCTCCCTTCTGTG
 ACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCCCCATCCGGCAAGCAGATAACCAAGGTTTAAACCATAGGA
 ATTCTGGTGAACATCCTGTGTCTTCTGCTGCCGATTTGTGGTTTATCTCAAAGGAAGACCTTGATACGACT
 GCTGTTTACAAATAAGAAGACCACCATTAAGGATTAAGGTTGTGTGCGGCCCTTCCCGGCCACCCCGTGGCTTCC
 AACCTGTGAGGCTCACCTCGGCCACCTTGGAAAAGGCTGTATGAGGAAGCCGCCAGATTCTTACCCACCGAAG
 GACAAATCCAGGAGATTGCTGCAGTGTGCAATGTTGACATCAGCAGACCCCTCAACGGCCTGAATGTCCCTCA
 GCCCCAGTCACTCAGCGAGTGTCTTCTCCCTCCACCGGGCCCCAGTGCACCTAGCGTCCCTGCCAGACCCC
 TGCCAGCCAAGCCTGCACTTAAGCAGGCCCCAGGGGACCTGTAAAGCCAAACCCCCCTCAGAGCCTCTGCCTGCA
 GATCCTCTGGCCAGAACAACTCGGCTCACTCATGCTTGGCCAGGACCCAGGACAAATGGGAGACTGGGCTCCG

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FIGURE 2B

CCTGGCACCCCTCAGACCTGCTCCACAATATCCACACCAAGTGCCCGAGATCCACCCACACCGCCTATATTAAAGT
GAGAAGCCGACACCTTTTTTCAACAGTGAAGACAGAAGTTTGCACTATCTTTCAGCTCCAGTTGGAGTTTTTTTG
 TACCAACTTTTAGGATTTTTTTTAAATGTTTTAAACATCATTACTATAAGAACTTTGAGCTACTGCCGTCAGTGC
 TGTGCTGTGCTATGGTGTCTGTCTACTTGCACAGGTACTTGTAAATTTATTAATTTATGCAGAATGTTGATTAC
 AGTGCAGTGGGCTGTAGTAGGCATTTTTTACCATCACTGAGTTTTTCCATGSCAGGAAGGCTTGTGTGCTTTTAG
 TATTTTAACTGAACCTTGAAATATCCTGCTTGATGGGATTCTGGACAGGATGTGTTTGCTTTCTGATCAAGGCCCTT
 ATTGGAAAGCAGTCCCCCACTACCCCGAGCTGTGCTTATGGTACCAGATGCAGCTCAAGAGATCCCAAGTAGA
 ATCTCAGTTGATTTTCTGCTTCCCCATCTCAGGCCAGAGCCAAGGGGCTTCAGGTCCAGGCTGTGTTTGGCTT
 TCAGGGAGGCTGTGCTGCTTGCACAACTGGCAGGCAGGCTCCCAGGGACACCTGGGAGAAATCTGGCTTCTGG
 CCAGGAAGCTTTGGTGAGAACCTGGGTTGCAGACAGGAATCTTAAGGTGTAGCCACACCAGGATAGAGACTGGA
 ACACTAGACAAGCCAGAACTTGACCTTGAGCTGACCAAGCCGTGAGCATGTTTGGAGGGGCTGTGATGTGCACT
 CAAGGCGGTGCTTGATAGAAATGCCAAGCACTTCTTTTTCTCGCTGTCTTTCTAGAGCACTGCCACCAAGTAGG
 TTATTTAGCTTGGGAAAGGTGGTGTCTCTGTAGAAACCTACTGCCAGGCACCTGCAAAACCGCCACCTCCCTAT
 ACTGCTTGGAGCTGAGCAAAATCACCACAACTGTAATACAATGATCCTGTATTCAGACAGATGAGGACTTTCCA
 TGGGACCACAACTATTTTCAGATGTGAACCTTAAACAGATCTAGTCAATCAAGTCTGTTTACTGCAAGGTTCA
 ACTTATTAACAATTAGGCAGACTCTTTATGCTTGCAAAAACTACAACCAATGGGAATGTGATGTTTATGGGTATA
 GTTCATGTCTGCTATCATTATTCGTAGATATTGGACAAAGAACCTTCTCTATGGGGCATCTCTTTTTTCCAACT
 TGGCTGCAGGAATCTTTAAAGATGCTTTTAAACAGAGTCTGAACCTATTTCTTAACACTTGCAACCTACCTGT
 TGAGCATCACAGAATGTGATAAGGGAATCAACTTGCTTATCAACTTCTTAAATATTATGACATGTGGCTTGGGC
 AGCATCCCCCTGAACTCTTCACTCTTCAAATGCTGACTAGGGAGCCATGTTTCACAAGGTCTTTAAAGTGACT
 AATGGCATGAGAAATACAAAATACTCAGATAAGGTAAGTAAATGCCATGATGCCCTGTGCTTCTGGACTGCTTTTC
 ACATTAGAAGACAATTGACAACAGTTACATAATTCACCTCTGAGTCTTTTATGAGAAAGCCTTCTTTTGGGGTCA
 ACAGTTTTCTATGCTTTGAAACAGAAAAATATGTACCAAGAACTCTTGGTTTGCCTTCCAGAAACAAAACCTGC
 ATTTCACTTCCCCGGTGTTCCTCACTGTATCTAGGCAACATAGTAATCATGACTATGGATAAACTAAACAGTG
 ACACAAACACACACAAAGGGGAACCCAGCTCTAATACATTCCTACTCGTATAGCBEGCATCTGTTTATTCTATA
 GTTATTAAGTCTTTAAATGTAAAGCCATGCTGGAAAAATAATCTGCTGAGATACATACAGAATTACTGTAAC
 TGATTACACTTGGTAAATGTACTAAAGCCAAACATATATATACTATTAAAAAGGTTTACAGAAATTTTATGGTGC
 ATTACCTGGGCATTGTCTPTTPTAGATGCCCAATCCTTAGATCTGGCATGTTAGCCCTTCTCCAAATTATAGA
 GGATATGAACCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 3

GGAGTTTCAAGAAGCGCTAGTAAGGTCTCTGAGATCCTTGCACTAGCTACATCCTCAGGGTAGGAGGAAGATG
GCTTCCAGARGCATGCGGCTGCTCCTATTGCTGAGCTGCCTGGCCAAAACAGGASTCCTGGGTGATATCATCAT
GAGACCCAGCTGTGCTCCTGGATGGTTTTACACAGTCCAAATTGCTATGGTTACTTCAGGAAGCTCAGGAACT
GGTCTGATGCGGAGCTCGAGTGTCTAGTCTTACGGAAACGGAGCCCACTGGCATCTATCCTGAGTTTAAAGGAA
GCCAGCACCATAGCAGAGTACATAAGTGGCTATCAGAGAGGCCAGCCGATATGGATTGGCCTGCACGACCCACA
GAAGAGGSCAGCACTGGCAGTGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGCAAGTCCATGGGTG
GGAACAAGCACTGTGCTGAGATTAGCTCCAATAACAACFTTTTAACTTGGAGCAGCAACGAATGCAACAAGCGC
CAACACTTCCTGTGCAAGTACGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTCTC
TTCTTTCTGCTAGCCTGGCTAAATCTGCTCATTATTTAGAGGGGAAACCTAGCBACTAAGAGTGATAAGGG
CCCTACTACACTGGCTTTTTTAGGCTTAGAGACAGAACTTTAGCATTGGCCCCAGTAGTGGCTTCTAGCTCTAA
ATGTTTGCCCCGCCATCCCTTTCCACAGTATCCTTCTTCCCTCCTCCCTGTCTCTGGCTGTCTCGAGCAGTCT
AGAAGAGTGCATCTCCAGCCTATGAARCAAGCTGGSTCTTTGGCCATAAGAAGTAAAGATTTGAAGACAGAGGA
AGAAACTCAGGAGTAAGCTTCTAGACCCCTTCAGCTTCTACACCTTCTGCCCTCTCTCCATTGCCCTGCACCCC
ACCCAGCCACTCAACTCCTGCTTGTFTTTCTTTGGCCATAGGAAGGTTTACCAGTAGAATCCTTGTAGCTT
GATGTGGGCCATACATTCTTTAATAAACCATTGTGTACATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 4

GGGGAGCAGAGAGGAGGCAATGSCCAACCATGGAGAACAGGTSATCTGGGCCCTGGTCCTGGTGTCCATGCTGG
CCCTCGGGCACCTTGGCCGAGGCCCAGACAGAGACGTGTACAGTGGCCCCCGTGAAAGACAGAAATTGTGGTTTT
CCTGGTGTACGCCCCCTCCAGTGTGCAATAAAGGGCTGCTGTTTOSACGACACCGTTGGTGGGGTCCCCTGGTG
CTTCTATCCYAAATACCATCGACGTCCCTCCAGAGAGGAGTGTGAATTTTAGACACTTCTGCASSEATCTGCCT
GCATCCTGACGCGGTGCCATCCCCAGCACCGTGATTAGTCCCAGASCTGCGCTGCCACCTCCACCGSACACCTC
AGACACGCTTCTGCAGCTGTGCTCGGCTCACACACAGATTGACTGCTCTGACTTTGACTACTCAAAATTGGC
CTAAAAATTAAAAGAGCTCGATATTAAAA

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FIGURE 5

AATCCATCTGAGAAATATGCTGCCACAAATACCCCTTTTCTGCTAGTATCCCTGAACCTTGGTTCATGGAGTGTTTTACGGCTG
 AACGATACCAAAACGCCACAGGCATAAAAGGCCACTACCCACACCCAGACACAGTTCTTCTTCCCTACACCAATAAGAG
 TAAAGGTATATGCAATAAGAGGAGAGCAAGGTACTCCTGGTCCACAGGCCCTGCTGGAGCTCGAGGCCACCCAGGTCCTTCT
 GGAACCCAGGAAACACAGGCTACGGAGTCTCTGGACTCCAGGAGAGGCCAGGGTTGCCAGGACCCAGGGACCAACAGCTG
 TAGGGAACACAGGTTGTGCCAGGACTCCAGGAAACACAGGAGAGAGGACCATATGGAACAAAGGAGATGTTGACCCAGC
 TGGCCTACAGGACCCCGGGCCCAACAGGACCACTGGAATCCTTGGACCCGCTGGATTTCTGTGCCAGGAAACCTGGA
 CAACAGGGACCCACAGGAGCCCCAGGACCCAGGGGCTTCTGGAGAAAGGGGTGCACCGAGAGTCCCTGGTATGAAATGGAC
 AGAAAGGGGAAATGGATATGGTCTCTCTGCTGCTCCAGGTGAGAGGGGTCTTCCAGGCCCTCAGGTCACACAGGACCATC
 TGGCCCTCCTGGAGTGGGAAAGAGGTGAAATGGGGTTCCAGGACAGCCAGGCATCAAGGTGATASAGGTTTTCCGGGA
 GAAATGGGACCAATTGGCCACAGGTCCCAAGGCCCTCCTGGGAGACAGGCCAGAGGCATTGGAAAGCCAGGAGCTG
 CTGGAGCCCCAGGCCAGGCCAGGATTCAGGAAACAAAGGTCTCCTGGGGTCCAGGATAGCTGGGCCCCAGGGCTCTC
 TGGCTTTGGAAACAGGCTTGCAGGCCCTGAGGGAGAAAGAGACCTGCTGGCCTTCTGGGGTCCAGGTGCCAAAGGG
 GAACAGGGCCAGCAGGCTTCTGGGAAGCCAGGCTCTACTGGACCCCTGGAATATGGGACCCCAAGGACCAAAAGGCA
 TCCGGGTAGCCATGCTCTCCAGGCCCTAAAGGTGAGACAGGGCAGCTGGCCTGCAGGATACCTGGGGCTAAGGGTGA
 AAGGGGTTCCTCTGGTCAATGGAAACAGGCTACCCAGGAAACAGGCTCTCATGGTCTTAAGGTAACCCAGGGTTA
 CCAGTCCAAAGGTGATCTCTGGAGTTGGAGGACCTCCTGCTCTCCAGGCCCTGGGGCCACAGGAGCAAGGGAATGC
 CCGGACACAATGGAGAGGTGGGCCAAGAGGTGCCCTGGAATACAGGTACTAGAGGCCCTATTGGGCCACAGGCATTCC
 AGGATTCCTGGGTCTAAAGGGATCCAGGAATGCCGGTCTCCTGGCCAGCTGGCAATGCACTAGGGGCTCAATGGA
 CCCACCGGCCACAGGGCTCCAGGTCCAGAGGCCCTCTGGAGAGCCCTGGTCTTCCAGGGCCCTGGGCTCCAGGCC
 CACCGGTCAAGCAGTCAATGCTGAGGCTTTTATAAAGGACAGGCCAAGGCCCGGCTTTCTGGGACCTCTTGTAGTGC
 CAACAGGGGGTAACAGGAATGCTGTGTCTGCTTTACTGTTATCTCTCCAAAGCTTACCCAGCATAGGAATCCCATTA
 CCATTTGATAAAATTTTGTATAACAGGCAACAGCATATGROCCAGGACTGGAACTCTTACTTGTCTAGATACAGGATAT
 ACTATTTTCTATACACGTGCATGTGAAGGGAATCATGTTTGGGTAGGCCCTGTATAAGAAAGGCCCTGTAAATGTACAC
 CTATGATGAATACACCAAGGCTACCTGGATCAGGCTTCCAGGAGTGCATCAATGATCTCCAGGAAATGACCAGGTGTGG
 CTCCAGCTTCCAAATGCCAGTCAATGGGCTATACTCCTCTGAGTATGTCCACACCTCTTCTCAGGATTCCTAGTGGCTC
 CATGCTGAGTACACCCACAGAGCTAATCTAAATCTTGTCTAGAAAGCATTCTCTAATCTACCCACCCCTACAAATG
 CATATGAGGTAGGCTGAAAGGAATGTAAATTTTATTTTCTGAAATACAGGTTTGAGCTATCAGACCAACAAACCTTCCCCC
 TGAABAGTGAGCAGCAACTAAACCTATGTGAAGCTCTCTTGAATTTCTAGTTCAGCATCTTAAGGCTCTTTAAGGTTT
 TCTCCAAATTTAAAAATATCACCAAGGAAGTCTTCTATGTTAAABCAACACAAABACAAAGCAACAAABAAAAA
 TTAABAAAAAACAAGAAATAGAGCTTAAGTTATGTGAATTTGATTTGAGAACTGGGCTTTCTTTTAAABAGGCT
 GTTTCTAATATGAATATGGAACCTCTAGGAACATCCAGGAGGTATCATATACTTTGTAGAACTTAAATCTTGAAAT
 TCAAAATTTAAAGACACTGATCCCCTAAATATTTCTGATGCTGCCTACTCTGAGGCCTGTATGGCCCTTTCTCAATA
 TCTATTCAAATATACAGGTGCATATATCTTGTAAAGCTCTTATATAAABAGCCCAAAATATTGAAGTTCACTCTGAAT
 GCAAGGTGCTTTCAATCAATGAACCTTTCAAACTTTCTATGATTCAGGAGAGCTTTTATATACCCAGCATACCTTGA
 AACAGGTATCTGACCTATTCTTATTTAGTTAACACAGGTGATTAATTTGATTTCTTTAATTCCTTATGAACTTATGTG
 ATATGATTTTCTGGATTTACAGAACATTACACATGTACCTTGTGCTCCCATTCAGTGAAGTTATAATTTACACTGAGGG
 TTTCAAAATTCGACTAGAACTGGAGATATATTTATTTATTTATGCACTGTACTGATTTTATATGCTGTATAAACTTTA
 AGCTGTGCTCACTTATTAAGACAAATGTTTTACCTACTCCTTATTTACGACACATAAAATAACATCAATAGATTTT
 AGGCTGAATTAATTTGAAGCAGCAATTTGCTGTTCTCAACCAATCTTTCAAGGCTTTCAATGACACATAAAATAACAT
 CATAGATTTTAAAGGATGGGTGGCTT

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FIGURE 6

CATGCCGCGCGCGCGCGCTGCTGCTGTTGCTCCTGGCGGGCGCCTTGGGGACGSSGCAGTTCCTGTGTCTCTGGTG
GTTTGCCTAAACCTGCAAACATCAOCTTCTTATCCATCAACATGAAGAATGTCTTACAATGGACTCCACCAGAG
GGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTATATATGGGCAAAAGAAATGGCTGAATAAATC
AGRATGCAGAAATATCAATAGAACCTACTGTGATCCTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATG
CCAAAGTTAAGGCCATTGCGGGAACAAAGTGTTCRAATGGGCTGAAAGTGGACGGTCTATTCCTTTTTTAGAA
ACACAAATTGGCCACCAGAGCTGGCACTGACTACAGATGAGAAGTCCATTTCTGTGTGCTGACAGCTCCAGA
GAAGTGGAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGAAGTATAACGTGT
CTGTGTTGRATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCCACAGCTGGTGTTCACCTGGCTG
GAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTTGGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGA
GAAGCAGTGTGCCAGGACTTTGAAAGATCAATCATCAGAGTTTCAAGGCTAAATCATCTTCTGTGTATGTTTTGC
CCATATCTATTACCGTGTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAG
AAACACCCAGCAAAATTTGATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCTGTGAAAAAT
CGTGATTAACCTTTATCACCTCAATATCTCGGATGATTTCTAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAGCAGTGTATGTATCCAGCCTTAATGATCCTCAGCCAGCGGGAACCTGAGSCCCCCCTCAGGAGGAAGAGGAG
GTGAAACATTTAGGGTATGCTTCGCAATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAGCTACTTC
TCTCACCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAAACAGTCATTGAATATGAATATGATGTCA
GAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAGGAACA
TTATTTGGASTCGCAGGCAGCCTTGGCAGTCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCA
AGACTTAGACCCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGSGCCGGAGGAAGAGCCATCGACGACCCCTGG
TCGACTGGGATCCCCAAACTGGCAGGCTGTGTATTCTTCTGCTGTCCAGCTTCGACCAGGATTGAGAGGGCTGC
GAGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAG
GCCACCGAGGAGAAATGAAACCTATCTCATOCAATTGATGGAGGAATGGGCTTATATGTGCAGATGGAAACT
GATGCCAACACTTCCTTTTTGCCTTTTGTTCCTGTGCAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAG
TAOCTGGGATGAAAGAAGTTTTTTCCAGTTTGTCACTGTCTGTGAGAA

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FIGURE 7

ASOGGGGCGTGGGACTGAGCAGTCTGCTGCCCCCGACATGTGACCCAGCCCCGCGGGCCATGCGGGGTCCCGGC
 CCCCCGGCCCTGCGGGCCGCTGCGGCTGCCGCGCTGCTGCTGTTGCTCCTGGCGGGCGCCTTGGSSAUCGGCCAGT
 TCCCTGTGTCTCTGGTGGTTTGCCTAAACCTGCAACATCACCTTCTTATCCATCAACATGAAGAATGTCTAC
 AATGGACTCCACCAGAGGGTCTTCAAGGACTTAAAGTTACTTACACTGTGCACTATTTTCAATATATGGSCAAAAG
 AATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTGTGATCTTTCTGCTGAAACTTCTGACTA
 CGAACACCAGTATTATGCCAAAGTTAAGGCCATTTGGGGAAACAAAGTGTTCAAATGGGCTGAAAGTGGACGGT
 TCTATCCTTTTTTASAAAACACAAATTTGGCCACCAGAGGTGGCACTGACTACAGATGASAGTCCATTTCTGT
 GTCTGACAGCTCCAGAGAAAGTGGAAACAGAAATCCAGAAGACCTTCCGTGTTCCATGCAACAAATATACTCCAA
 TCTGAAGTATACCGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGCTCCAGTGTGTGACCAACCAACCGC
 TGGTGTCTACCTTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTTCGTCCCAGGGCCCCCTCGC
 CGTGTCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCATCAGAGTTCAGGGCTAABATCAT
 CTCTGTGTATGTTTTGCCCATATCTATTACCSTGTTTCTTTTTCTGTGATGGGCTATTCCATCTACCGATATA
 TCCACGTTGGCAAAGAGAAACACCCAGCAATTTGATTTTGAATTTATGCAATGAATTTGACAAAAGATTCTTT
 GTGCCGTGCTGAAAAAATCGTGATTAACFTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
 TATGAGTTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCCAGCGGGAACCTGAGGCCCC
 CTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAA
 AACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGA
 RTATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAGAGAGCAGGAGCTCAGTTTTCAGGAGGAGG
 TGTCCACACAAGGAACATTATTGGAGTCCGAGGCAGCGTTGGCAGTCTTGGGCCCCCAAACGTTACAGTACTCA
 TACACCCCTCAGCTCCAAAGACTTAGACCCCCCTGGCGCAGGAGGCACACAGACTCGGAGGAGGGGCGGAGGAAGA
 GCCATCGACGACCCCTGGTCCACTGGGATCCCCAAACTGGCAGGCTGTGTATTCCTTCCTGTCCAGCTTCGACC
 AGGATTCAGAGGGCTGCCAGCCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAG
 GAGCCGGCTCCAGACAGGCCACCGAGGAGAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTATA
 TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTCTCTGTGCAACAAGTGAGTCACCCCTT
 TGATCCAGCCATAAAGTACCTGGGATGAAAGAGTTTTTCCAGTTTGTCASTGTCTGTGAGAA

FIGURE 8

[illegible]

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FIGURE 9

GAAGGACAGCAGGGCCACAGTCCACAGCAGCCCTGACCAGAGCATTCTTGGAGCTCAAGCTCCTCTACAAAGAG
 GTGGACAGAGAAGACAGCAGAGACCATGSGGACCCCCCTCAGCCCCCTCCCTGCAGATTGCATGTCCCTGGAAAG
 AGGTCTCTCTACAGCCCTCACTTCTAACCTTCTGGAAACCCACCCAGCACTGCCAAGCTCACTATTGAATCCACG
 CCGTTCAATGTCCAGAGGGGAAGGAGGTTCTTCTACTCGGCCACAACCTGCCCCAGAATCGTATTGGTTACAG
 CTGGTACAAAGCCGAAAGAGTGGATGGCAACAGTCTAAFTGTAGGATATGTAAATAGGAACTCBACRAGCTACCC
 CAGGGCCCCGCATACAGTGGTCCGAGAGACAATATACCCCAATGCATCCCTGCTGATCCAGAAGCTCAGCCAGAAAT
 GACACAGGATTCTATACCCCTACAAGTCATAAAGTCAGATCTTGTGAATGAAGAAGCRAACGGACAGTTCCATGT
 ATACCCGGAGCTSCCCAGCCCTCCATCTCCAGCAACAACCTCCACCCCGTGGAGGACAAGGATGCTGTGGCCT
 TCACCTGTGAACCTGAGGTTCAGACACACAACCTACCTGTGGTGGGTAAATGGTCAGAGCCTCCCGGTCACTCCC
 AGGCTGCAGCTGTCCAATGGCAACATGAACCTCACTCTACTCAGCGTCAAAAGGAACGATGCAGGATCCTATGA
 ATGTGAAATACAGAACCCAGCGAGTGGCAACCCGAGTGAACCCAGTCAACCTGAATGTCTCTATGGCCAGATG
 GCCCCACCATTTCCCCCTCAAAGGCCAATTACCGTCCAGGGGAAAATCTGAACCTCTCCTGCCACGCAAGCTCT
 AACCACCTGCACAGTACTCTTGGTTTATCAATGGGACGTTCCAGCAATCCACACAAGAGCTCTTTATCCCCAA
 CATCACTGTGAATAATAGCGGATCCTATATGTGCCAAGCCCACTAAGTCAAGCCACTGGCCTCAATAGSACCCAG
 TCAGGATGATCAGCTCTCTGGAAGTGTCTCTCTCTCAGCTGTGGCCACCGTCCGGCATCAGGATTGGAGTG
 CTGGCCAGGGTGGCTCTGATATAGCAGCCCTGGTGTATTTTGGATATTTCAAGGAAGACTGGCAGATTGGACCAAG
 ACCCTGAATTCTTCTAGCTCCTCCAAATCCCATTTTTATCCCATGGGAACCACTAAAAACAAGGCTCTGCTCTCTCC
 TGAAGCCCTATATGCTGGAGATGGACAACCTCAATGAAATTTAAAGGGAAAACCCCTCAGGCCTGAGGTGTGTGC
 CACTCAGAGACTTCACCTAAGTACAGAGACAGGCCAACTGCAACCCATGGTGACAAATTGACCACTTCACACTATG
 GACAGCTTTTCCCAAGATGTCAAAACAAGACTCCTCATCATGATAAGGCTCTTACCCCTTTTAAATTTGTCTCT
 GCTTATGCTCTGCTCTTTTGGCTTGGCAGGATGATGCTGTGCTTACTATTTTCAACAAGATAGCTTCAGAGGGTA
 ACTTAACAGAGTATCAGATCTATCTTGTCAATCCCAACGTTTTTACATAAAATAAGAGATCCTTTAGTGCACCCA
 GTGACTSACATTAGCAGCATCTTAAACACAGCCGTGTGTTCAAAATGTACAGTGGTCCCTTTTACAGATTGGACTT
 CTAGACTCACCTGTTCTCACTCCCTGTTTTTAATTCAACCCAGCCATGCAATGCCAAATAATAGAAATTGCTCCCT
 ACCAGCTGAACAGCGAGGAGTCTGTGCACTTTCTGACACTTGTGTTGTAACATGGCTAAATACAAATGGGTATCG
 CTGAGACTAAATTTGTAGAAATTAAACAATGTGCTGCTTGGTTAAATGGCTFACACTCATCTGACTCATTTCTTA
 TTCTATTTTACTTGGNTTGTATCTTGCCTAAGGTGGGTAGTCCAACTCTTGGTATTTACCCCTCCTAATAGTCATA
 CTAGTAGTCATACTCCCTGGTGTAGTGTATTTCTTAAAGCTTTAAAGTCTGCAATGCAGCCAGCCATCAATA
 GTGAATGGTCTCTCTTTGGCTGGAAATTACAAAACCTCAGAGAAATGTGTCAACAGGAGAACATCATAACCCATGA
 AGGATAAAAGCCCCAATGGTGGTAACTGATAATAGCACTAATGCTTTAAGATTGGTCACTCTCACCTAGG
 TGAGCGCATTSAGCCAGTGGTGCATAAATGCTACATCTCCAATGAATSTTAAGGAAGAAGATAGATCCAAAT
 TAAAAAAATTAACCAATTTAAAAAAAGAAACACAGGAGATTCCAGTCTACTTGAGTTAGCATAATACA
 GAATCCCCCTCTACTTTAACTTTTACAAAAAGTAACCTGAACATACTGTATGTTAACCAATGTATTTATTTCT
 GTGGTTCTGTTTCTTCTTCCAAATTTGACAAAACCCACTGTTCTTGTATTGTATTGCCAGGGGGAGCTATCAC
 TGTACTTGTAGAGTGGTGTCTTAAATCATAAATCAAAATAAAGCCAATTAGCTCTAAAAA

GAUCCUGGGGGGGCGAGGGGCCCCCAAACTCAGTTCCGATCCTACCCGAGTGAGGGCGGCGCCATGAGAGCTCCGGG
TGCTGCTCTGCTGGGCTTCGTTGGCCGCGAGCTTTGGAAGAGACCTGCTGAACACAAAATTCGAAACTGCTGAT
CTGAAGTGGGTGACATTCCTCAGGTGGACGGGCACTGGGAGGAAGTGAAGCGGCTGGATGAGGAACAGCACAG
CGTGGCCACCTACGAAGTGTGTGACGTGACAGCGTGGCCCGGGGCGAGGCGGCTGGCTTCGACAGGTTGGGTCC
CACGGCGGGGGCGCGTCCAGCTGTACGCCACGGCTGGGCTTCACCATGCTCGAGTGGCTGTCCCTGGCTCGGGCT
GGGCGCTCCTGCAAGGAGACCTTTCACCGTCTTCTACTATTGAGAGCGATGCGGACACGGCCAGGGCTCTACGGC
AGCTCTGGATGGAGAACCCCTACATCAAGTGGAGACGGTGGCGCGGAGCATCTCACCCGGAAGCGGCTGGGG
CGAGGGCCACCGGGGAAGGTGAATGTCAAGACGCTGGGTCTGGGACCGCTCAGCAAGGCTGGGCTTCTACCTGGCC
TTCCAGGACACAGGCTGGCTGCAATGGGCTGCTATCCCTGACCTCTCTCTACAAAAAGTGGCGCCAGCTGACTGT
GAACCTGACTCGATTCCCGGAGACTGTGCCTCGGAGCTGGTGTGGCCCTGGCCGGTAGCTCGCTGGTGGATG
CGGTGGCCCGGGCTGGGCGCCAGCGCCAGGCTCTACTGGCGTGAGGATGGCCAGTGGGCGGAACAGCGGCTCAG
GGTGTGAGCTGTGCTCGGGGCTTCGAGGCGAGCTGAGGGGAAACCAAGTCCCGAGCTGTGGCAGGGCTT
CAAGCCCTGTGTCAGGAGAAAGGTTCCTGCGAGCATCGCCAGCCATAGCCATCTAACACCTTGGATCAGCGG
TCTGCGAGTGGCGCTGGGTCTGGGTCTCGGGGACGACAGACCGCCCGGGGCTGACCTCTGACCCACCGCTCTCG
GCTCGGGGAGCGTGGTTTCCCGCTGAAAGGCTCTCTGCTGACCTGGAATGGAGTGGCCCGCTGGAGTCTGG
TGGCGGAGAGGACCTCAGCTACGGCTCTCGCTGCGGGGAGTGGCGACCTGGAGGCTCTGTGGCGCTGGGGG
GAGACCTGACTTTTGACCGCGGGCGCGGGGAGCTGGTGGAGCGCTGGGTGGTGGTTCGAGGGCTACCTCTGAC
TTCACCTATACCTTTGAGGTGACATGCAATGAAACGGGCTATCTCTTACCCAGCGGGCGCTCTCAATTTGAGCC
TGTCAATGTCACCACTGACCGGAGAGGTACCTCTCGAGTGTCTGACATCGGGTGAAGCGGCTCTCACCGAGCA
GCTTGAGCTGTGGCTGGCTGCTTTCGCGGCGGACCGGAGTGGGCTGTGCTGGACTACGAGTCAAAATACCATGAG
AAGCGCGCGGAGGCTCCAGCAGGCTGGGTTCTGAGAGCTCAGAAAAACCGGGCAGAGCTGGGGGGCTGAA
GGGGGAGCCAGCTACCTGGTGGAGTACGGGCGGCTCTGAGCGGGCTACGGGGCTTCGGCCAGGAACATC
ACAGCCAGACCCAACTGGATGAGAGCGAGGCTGGCGGGAGCAGCTGGCGCTGATTGGGGGACGGGCGAGTGGT
GGTGTGGTCTGGTCTGTGGTCTATTGTGGTGGAGTCTCTGCTGCTCAGGAACAGAGACCTGGGAGAGAAG
AGAATATTCGGACAAACAGGACAGTATCTCATCGGACATGGTATAGGCTACATCGACCTCTGATATG
AAGACCTTAATGAGGCTGTGAGGGAATTTGCAAAAGAGATCGATGTCTCTAGTCAAGATTGAAGAGTGTATT
GGTGCAGTGTGAGTTTGGCGAGGTGTGTGGGGGGGCTCAGGGCGGCGGAGGAAGAGAGAGCTGTGTGGCAAT
CAAGACCTGGAAGGCTGGCTACACGGAGCGGCGAGCGGCTGGGTTTCTGAGCGAGGCTCTCATCATGGCCAGT
TCGAGCACCCCAATATCATCGGCTGGAGGGCTGGTCAACAACAGCATGGCGCTCATGATTCTCACAGAGTTC
ATGGACAACGGCGGCTGGAGTCTCTCTCGGCGTAAACGACGGACAGTTCACAGTCTACAGCTCTGGTGGGCT
GCTCGGGGCGATCGCTCGGGGCTGGGCTACCTTGGCGAGATGAGTACGCTCCACCGAGAGCTGGGCTCTGGCA
ACATCTCTAGTCAACAGCAACCTCGTCTGCAAGTGTCTGACTTGGGCTTTCCGAGTTCTGGAGGAGAGCTCT
TCGATCCAGCTCAGCGAGCTCTCTGGGAGGAGAGATCCCATCGATGAGTGGCGCGGAGGCGATTGGCTT
CGGAGAGTTCACTTCCGCGAGTGATGGTGGAGTTACGGGATTGTGATGTGGGAGGTGATGTCAATTTGGGGAGA
GGCGTACTTGGGACATGAGCAATCAGGACGTGATCAATGCCATTGAACAGGACTACCGGCTGGCGCGCGGCGCA
GACTGTCCACCTCTCTCCACAGCTCATGCTGGAGTGTGGCAGAAAGACCGGAATGGCGGCGCGGCTTCC
CCAGGTGGTCAGCGGCTGGACAGATGATCCGGAACCGCGGAGCTCAAAATCGTGGCGGGAGAGATGGG
GGGCTTCACACCTCTCTCTGGACAGCGGCGAGCTCTACTCAGCTTTTGGCTGTGGCGGAGTGGCTTGG
GCCATCAAAATGGAGATACGAAGAAAGTTTCCGAGCGCTGGCTTTGGCTCTTGGAGTGGTCAAGCAGAT
CTCTGCTGAGGAGCTGCTGGCAATCGGAGTCACTCTGGCGGACACCCAGAGGAATCTTGGCAGTGTCCAGC
ACATGAAGTCCAGGCCAAGCGGGGAACCGGGTGGGACAGGAGGACCGGCGCGGAGTACTGAGCTGCAGGA
ACTCCCCACCCAGGGACACCGCTCTCCCATTTTCCGGGCGAGAGTGGGAGTCAAGAGGCCCCCAGCGCTGT
GCGCGCTGGATTGCACTTTGAGCGCGTGGGTTGAGGAGTTGGCAATTTGGAGAGACAGGATTTGGGGTTCTG
CCATAATAGGAGGGGAAAACTACCCCCCAGCCACTCGGGAATCCAGACCAAGGCTGAGGGCGCTTTCCCT
CAGGACTGGGTTGACACAGAGCAAGAGAGGAGTGGCAATCTCCAGCTCCAGAGTGGGGGGGCTGTCCAGGGG
ATGGCTGGTTTCCCGCAGACCAAGAGAGTGTGACTCCCTTGGCAGCTCCAGAGTGGGGGGGCTGTCCAGGGG
CGAAGAAGGGGTGTCCAGGGCCAGTGACAAATCAATTTGGGTTTGTAGTCCCACTTGTGCTGTCAACCCAA
ACTCAATCAATTTTTTCCCTTGTAAATGCCCTTCCCGCAGTCTGCTGCTTCAATATGAAGGTTTTGAGTTTTG
TTTTTGGTCTTAATTTTCTCCCGGTTCCCTTTTTTGTCTTCTGATTTTGTTTTCTACCGTCTTGTGATAACT
TTGTGTTGGAGGGAGCTGTTTCACTATGGCTCTCTTGGCCAAAGTTGAACAGGGGCCCATCATCTGTCTGT
TTCCAGAACAGTGGCTTGGTCACTCCACATCCCGGACCGCGCTGGGAGCCCCCAGCTGTGTCTATGAAGG
GTGTGGGCTGAGGTACTGAAAGGGCGGTAGTTGGTGGTGGGAACCCAGACCGGACCGGCTGTGGAGGGT
TCTTAAATTAATTTAAAAAGTAACTTTTTGTATAAATAAASAAAATGGGAGCTGTCCCAAAAAAAAAAAAAA
AAA

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FIGURE 11

[illegible]

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FIGURE 12

TGTGGGACTGCTTGGGTACCCBACCCAGCCCTGGGTAGCCTGCAGCAATGGGCCCAGCTGTTCCTGCCCCCTGCTG
 GCAGCCCTGGTCTTGGCCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAGAGGACCCGCGC
 TTTTCGGCTGGCCATCGCGGGCGACGGGCACTGCAGGGCCTGCTCGGCGGCGCCCTCACCATCCCTTGCCACG
 TCCACTACCTGCGGCCACCGCGAGCCGCGGCTGTGCTGGGCTCTCCGCGGGTCAAGTGGACTTTCCTGTCC
 CGGGGCGGGGAGGAGGCTGCTGGTGGCGGGGAGTSCGCTCAAGGTGACGAGGCTTACCSTTCCGGCT
 GGGACTGCTTGGTACCCAGCGCTCGCTCACCAGCTCTCCCTGGGCTGAGCGAGCTGGGCCCCAACGACTCAG
 GTATCTATCGCTGTGAGGTCCAGCACGGCATCGATGACAGCAGCGACGCTGTGGAGGTCAAGGTCAAGGGGTC
 GTCTTTCTCTACCGAGAGGGCTCTGCCGCTATGCTTTCTCTCTTTCTGGGGCCCCAGGAGGCTGTGCCCCGAT
 TGGAGCCACATCGCCACCCCGGAGCAGCTCTATGCCGCTACCTTGGGGGCTATGAGCAATGTGATGCTGGCT
 GGCTGTGGATCAGACCTGAGGTATCCATCCAGACCCACGAGAGGCTGTACGGAGACATGGATGGCTTC
 CCGGGGGTCCGGAATATGGTGTGGTGGACCCGGATGACCTCTATGATGTGTACTGTTATGCTGAAGACCTAAA
 TGGAGAATTGTTCTGGGTGAUCCCTCCAGAGAAAGCTGACATTGGAGGAAGCACGGGGCTACTGCCAGAGCGGG
 GTGCAGAGATTGCCACCAUCCGCTCACTGTATGCAGCTGGGATGCTGGCTGGACACTGCAGCCAGGGTGG
 CTAGCTGATGGCACTGTGGCTACCCCATCGTCAACCCAGCCAGCGCTGTGGTGGGGGCTTGGCTTGTGTCAA
 GACTCTCTTCTCTTCCCAACAGACTGGCTTCCCAATAAGCACAGCCGCTTCAACGTCTACTGCTTCCGAG
 ACTCGGCCCCAGCTTCTGCCATCCCTGAGGCTTCCAACCCAGCCCTCCAACCCAGCCTCTGATGGACTAGAGGCT
 ATCGTCAAGTGCAGAGACCCCTGGAGGACTGCAGCTGCTCAGGAAGCCACAGAGAGTGAATCCCGTGGGGC
 CATCTACTCCATCCCATCATGGAGGACCGAGGAGGTGGAAGCTCCACTCCAGAGAGCCAGCAGAGGCCCTA
 GGAAGCTCTTAGAATTTGAACACAAATCCATGGTACCGCCACGGGCTTCTCAGAGAGGAAGGTAAAGCATTG
 GAGCAAGAAGASAAATATGAAGATGAAGAAG
 TCTGTGGGCTAGCCCCAGGAGCTCAGCAGCCCGGGGCTTGGAGGCTCTCTCCCCACTGAGCCAGCAGCCCCAGG
 AGGAGTCACTCTCCCAGGCGCCAGCAAGGGCACTCCTGCAGCCTGGTGCATCAACCTTCTGATGGAGAGTCA
 GAAGCTTCCAGGCTTCCAGGGTCCATGGAGCCACTACTGAGACTCTGCCACTCCCAGGGAGAGGAACCTAGC
 ATCCCCATCAGCTTCCACTCTGGTGGAGCAAGAGAGGTGGGGGAGGCACTGGTGGTCTGAGCTATCTGGGG
 TCCCTCGAGGAGAGAGCGAGGAGACAGGAAGCTCCGAGGGTGGCCCTTCCCTGCTTCCAGCCACACGGGCCCCF
 GAGGGTACCCAGGAGCTGGAGGCCCCCTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGGAGCTCAGTGCA
 GGGCCAGGAGTGTGCCCCACTGACAGCGCCAGCCGAGGTGGAGTGGCCGTGGTCCCCGCTCAGGTAAATCTG
 CCCAAGGCTCAACTGCCCCCTCTATCTACTCCTTTTCTTCCCCCTGCAGCTCTGGGTCACTTGAACCTGTAGTC
 CTTTAACCCACCATCATCCCAABCTCTCTCTCTTTTCCCTTCAATCTCTTACCCACCTCTACCTATGGGTCTC
 CAATCTCGGATATCCACCTTGTGGGTATCTCAGCTCTCGGCGTCTTTACCTGTGATCCAGCCCCGCGCACTGA
 CCATCTGTGACCCCTTCCCTGCCATGGGCCCCACCTGTGGCTCACATCTCGCCAGCCCCACAGAGCATCTC
 AGGCTCTCTCAGGGTCTCTCACTATTCAGGCTTCAAGGCTCGGCTTATTTCCACTACTCCCTTCATCC
 GCTGTGTGGCTTCCCCCTTAGCTGCTCTATTCATCTCAGGGAGGCTGGGAGTCCCTTCTCACCCCTCAAC
 CTCCGGAGTCCAGSAGAACCCGTACCCCCACAGAGCTTAAGCACTACTTCTGTGAAGTATTTTTTGTGTGT
 TCATGGAAACAAGCCTTGGAAATAATCTCTATTAACCGC

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FIGURE 13

AGCCAGCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCGGCCAGTGGGTAAATCGCCCTGGCCTTGGCTGC
CCTCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCAGGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAAC
ACATGGTAGAGTCTCCAACTGTTCACAGATGTCCAACTGCTCTGCGGCACTGATGGGCTCACATATACGAAT
GAATGCCAGCTCTGCTTGGCCCGGATAAAAAACCAACAGGACATCCAGATCATGAAAGATGCCAAATGCTGATC
CCACAGGAGCACCTCAGCCATGAAGTGTCAAGCTGGAGAACAGTGGTGGGCATGGAGAGGATATGACATGAAAT
AAAAGATCCAGCCCAAAAAAAAAAGAAAAA

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FIGURE 14

CGTTTCCAATGCACGTACAGCCCGTACACACCGTGTGCTGGGACACCCACAGTCAGCCGCAATGGCTCCCCCTGT
GCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCCCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTG
CTGCTTCTGCTGCTGTCCATCCCCAGAGGTTGCCCGGATGTCAGGAGGATTCCCCCTGGGAGGAGGCTCTTC
TGGGGAAGATGACCCACTGGGCGAGGAGGATCTGCCCACTGAAGAGGATTCACCCAGAGAGGAGGATCCACCCG
GAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCTAAATCAGAA
GAAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTCCTGGAGATCCTCAAGAACCCAGAAATA
TGCCCAAGAGGACAAAGAAGGAGGATGACCAAGATCATTTGGCGCTATGGAGGCGACCCGCCCCGGCCCCGGGTGT
CCCCAGCCTGCGCGGGGCGCTTCCAGTCCCCGGTGGATATCCGCCCCAGCTCCCGCCCTTCTGCCCCGGCCCTG
CGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCCCGCTCCAGAACTGGCGCTGCGCAACAATGGCCACAGTGT
GCAACTGACCCCTGCTCCTGGGCTAGAGATGGCTCTGGGTCCCGGCGGGAGTACCGGGCTCTGCAGCTGCATC
TGCACCTGGGGGCTGCAAGTCTGTCGGGCTCGAGACACTGTGGAGAGGCAACCGTTTCCCTGCCGAGATCCAC
GTGCTTCACTCAGCACCGCCTTTGCCAGATTTGACGAGGCTTGGGGCGCCCCGGGAGGCTGGCCGTTGTTGGC
CGCCTTTCTGGAGAGGGCCCCGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAGAAATCGCTG
AGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACCTCTGCTGCTGACTTCAGCCGCTACTTC
CGATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGTCTCTGACTGTGTTTAAACAGACAGTGAT
GCTGAGTGTCTAAGCAGCTCCACACCCCTCTCTGACACCTGTGGGGACCTGGTGAATCTCGGCTACAGCTGAAT
TCCGAGCGACCGAGCCTTTGAATGGGCGAGTCAATTGAGGCTCCTTCCCTGCTGGAGTGGACAGCAGTCTCGG
GCTGCTGAGCCAGTCCAGCTCAATTCTGCTGGCTGGCTGCTGCTGACATCCTAGCCCTGCTTTTGGCCTCCTTTT
TGCTGTCAACAGCGTCCGCTTCTGTGAGATGAGAAGCGAGCACAGAGGGCAACCAAGGGGCTGTGAGCT
ACCGCCCGAGCAGAGGTACCCGAGACTGGAGCCTAGAGGCTGGATCTTGAGAAATGTGAGAGGCCAGCCAGAGGC
ATCTGAGGGGAGCGGTAAGTGTCTCTGCTCATTTATGCCACTTCTTTTAACTGCCAAGAAATTTTATA
AAATAAATAATTTATAATA

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FIGURE 15

TCCACATCCAGGTCCTTGTGCTCCTCGCTTGCCTGTTCCCTTTTCCACGCATTTTCCAGGATAACTGTSACTCCA
 GGGCCCGCAATGSAATGCCCTGCAACTAGCAAAATTCGGCTTTTGCCGTTGATCTGTTCAAACAACATATGTGAAAAG
 GAGCCACTGGGCAATGTCTCTCTCTCCAATCTGTCTCTCCACCTCTCTGTCACTTGCTCAAGTGGGTGCTAA
 AGGTGACACTGCAAAATGAATTTGGACAGGTTCTTCATTTTGAAAATGTCAAAGATGTACCCCTTTGGATTTCAAA
 CAGTAACATCGATGTAAACAAACTTAGTTCCCTTTTACTCACTGAABCTAATCAAGCGGCTCTACGTAGACAAA
 TCTCTGAATCTTTCTACAGAGTTCTATCAGCTCTACGAAGAGACCGTATGCAAAGGAATTGGAACTGTTGACTT
 CAAAGATAAATTGGAAAGAAACGAAGGTCAAGTCAACAACCAATTAAGGATCTCACAGATGGCCACTTTGAGA
 ACATTTTAGCTGCAACAGTGTGAACGACCAGAACCAAAATCCTTGTGCTTAATGCTGCCTACTTTGTTGGCAAG
 TGGATGAAGAAATTTCTGAATCAGAAACAAAGATGTCTTTAGAGTCAACAAGACAGACCCAAACCACT
 GCAGATGATGAACRTGGAGGCCAGTTCTGTATGGGAAACATTGACACTATCAATTGTAAGATCATAGAGCTTC
 CTTTTCAAAATAAGCATCTCAGCATGTTCTATCCTACTACCCAAGGATGTGGAGGATGAGTCCACAGGCTTGGAG
 AAGATTGAAAAACAACCTCAACTCAGAGTCACTGTACAGTGGACTAATCCCAGCACCATGGCCATGCCAAGGT
 CAAACTCTCCATTCCAAATTTAAGGTGGAAAAGATGATTGATCCCAGGCTTGTCTGGAATCTAGGGCTGA
 AACATATCTTCAGTGAAGACACATCTGATTTCTCTGGAATGTGAGAGACCAAGGGAGTGGCCCTATCAATGTT
 ATCCACAAGTGTCTTAGAAATAACTGAAGATGGTGGGGATTCCATAGAGGTGCCAGGAGCAGGGATCCTGCA
 GCACAAGGATGAATTGAATGCTGACCATCCCTTTATTTACATCATCAGGCACAAACAAACTCGAATCATCAATTT
 TCTTTGGCAAAATCTGTTCTCCTTAAAGTGGCATAGCCCATGTTAAGTCCCTCCCTGACTTTTCTGTGGATGCCGA
 TTTCTGTAACTCTGCATCCAGAGATTCATTTCTAGATACAATAAATTGCTAATGTTGCTGGATCAGGAAGCC
 GCCAGTACTTGTATATGTAGCCTTCACACAGATAGACCTTTTTTTTTTTTCCAAATCTATCTTTTGTTCCTT
 TTTTCCCATAGACAATGACATACGCTTTAATGAAAAGGAATCACCTTAGAGGAAAAATATTTATTCATTTATF
 TGTCAAATTTCCGGGTTAGTTGGCAGAAATACAGTCTTCCACAAGAAAAATTCCTATAAGGAAGATTTGGAG
 CTCTTCTTCCAGCACTATGCTTTCTTCTTTGGGATAGAGAATGTTCCAGACATTCTCGCTTCCCTGAAAGAC
 TGAAGAAAGTGTAGTGCATGGGACCCACGAACTGCCCTGGCTCCAGTGAATCTTGGGCACATGCTCAGGCTAC
 TATAGGTCCAGAACTCCTTATGTTAAGCCCTGGCAGGCAGGTGTTTATTAATCTGAAATTTTGGGATTTTC
 AAAAGATAATATTTTACATACACTGTATGTTATAGAACTTCATGGATCAGATCTGGGSCAGCACCCCTATAAATC
 AACRCCTTAATATGCTGCAACAAAATGTAGAATATTCAGACAAAATGGATACATAAAGACTAAGTAGCCCATAA
 GGGGTCAAATTTGCTGCCAAATGCGTATGCCACCAACTTACAAAACACTTCGTTCCGAGAGCTTTTCAGATT
 GTGGATGTTGGATAGGAATTATAGACCTCTAGTAGCTGAAATGCAAGACCCCAAGAGGAAGTTAGATCTTA
 ATATAAATTCATTTTCAATTTTGTATAGCTGTCCCATCTGGTCAATTTGTTGGCACTAGACTGGTGGCAGGGCT
 TCTAGCTGACTTGACAGGGATTCTCACAATAGCCGATATCAGAATTTGTGTTGAAGGAACCTTGCTCTTTCATC
 TAATATGATAGCGSGABAAGGAGAGGAACCTACTGCCCTTAGAAAATATAAGTAAAGTGATTAAGTGCTCAG
 TTACCTTGACACATAGTTTTTCACTCTATGGGTTTAGTTACTTTAGATGGCAAGCATGTAACCTTATATTAATAG
 TAATTTGTAAAGTTGGTTGGATAAGCTATCCGTGTTGCAGGTTTATGGATTACTTCTCTATAAAAAATATGTAT
 TTACCAAAATTTTGTGACATTCCTTCTCCATCTCTTCCCTGACCTGCATTGTAAATAGGTTCTTCTTGTCTC
 GAGATTCAATATTGAATTTTCCCTATGCTATTGACAATAAAATATTATTGAACCTACA

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FIGURE 16

GCCGAGCCGGGGCTCCGGAAGCCGGCCGGGGCGCCGCGGCCGCTGCGGGGCGTCAATGGATCGCCACTCCAGCTA
CATCTTCATCTGGCTGCAGCTGGAGCTCTGCGCCATGGCCGTGCTGCTCACCAGGTTGAAATTCGATGCTACT
GTGATGCTGCCCCACTGTGTAGCCACTGGTTATATGTGTAATCTGAGCTCAGCGCCTGCTTCTCTAGACTTCTT
GATCCTCAGAACTCAAATTCGCCACTCACCCATGGCTGCCGTGGACTCTCTTGCAAGCACGACAGACATCTGCCA
AGCCAAACAGGCCCCGAAACCACCTCTGGCACCACCATACCCACATGGCAATGCTGTCTATGAAGACATGTGCAAT
ACAGAGGGGCTGCAGATGTTCTCTCTCCTCCAGGGGTGAGGCCTCAGGACAAGGAAACAGGTATCAGCATGAT
GGTAGCAGAAACCTTATCACCAAGGTGCAGGAGCTGACTTCTTCCAAAGAGTTGTGGTTCCGGGCGCGGTCAT
TGCCGTGCCCCATGCTGGAGGGCTGATTTTGTGTTGCTTATTATGTTGGCCCTGAGGATGCTTCGAAGTGAAA
ATAAGAGGCTGCAGGATCAGCGGCAACAGATGCTCTCCCGTTTGCACTACAGCTTTCACGGACACCATTCCAAA
AAGGGGCGAGTTGCAAAATAGACTTGGAAATGCATGGTGCCGGTCAGTGGGCAAGAGAACTGCTGTCTGACCTG
TGATAAAATGAGACAAGCAGACCTCAGCAACGATAAGATCCTCTCGCTTGTTCACTGGGGCATGTACAGTGGGC
ACGGGAAGCTGCAATTCGTATGACGGAGTCTTATCTGAAGTACACTTACTGAACAGCTTGAAGGCCCTTTTGAGT
TCTGCTGGACAGGACCACTTTATCTGAAGACAACTCATTTAATCATCTTTGACAGACAAATGACCTCTGCAA
ACAGAATCTTGGATATTTCTTCTGAAGGATTATTTGCACAGACTTAATACAGTTAAATGTCTTATTTGCTTTT
AAAATTATAAAAAGCAAAGAGAGACTTTGTACACACTGTCCACAGGGTTATTTGCATCCAGGGAGCTGGAAT
TGACTACCTAAATAAACAAAAATGTGCCCTAAAAA

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FIGURE 17A

GTCACCTTAGGAAAAGGTGTCTCTTCGGGCAGGCGGCTCAGCATGAGGAACAGAGGAATGACACTCTGGACAG
 CACCCCGGACCCCTGTACTCCAGCGGCTCTCGGAGCACAGACTTGTCTTACAGTGAAAGCGACTTGGTGAATTTTA
 TTCAAGCAAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAGATTCCAAGGCCACGGAGAATGTGTGCAAG
 TGTGGCTATGCCCAGAGGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAATGGAACACAGAAACA
 CACCAAGGAATTTCTACCGACGCTTTGGGGATATTCASTTTGAGACACTGGGGAAGAAGGGAAGTATATAC
 GTCTGTCTCTCGACACGGACGCGGAATCCTTTACGAGCTGCTGACCCAGCACTGGCACCTGAAACACCCAC
 CTGGTCATTTCTGTGACCGGGGGGCGCAAGAACTTCGCCCCGAGGCCGCGCATGCGCAAGATCTTCAGCCGGCT
 CATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCAGGGAGGCACCCATTATGGCCTGACGAAGTACATCG
 GGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCAGAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGG
 GGCATGGTCTCCAACCGGGACACCTTCATCAGGAATTGCGATGCTGAGGGCTATTTTTTAGCCCACTACCTTAT
 GGATGACTTCACAAGGGATCCACTGTATATCCTGGACAACAACBCACACACTTGTCTGCTCGTGGACAATGGCT
 GTCATGGACATCCCACTGTGGAAGCAAGCTCCGGAATCAGCTAGAGAAGCATATCTCTGAGCGCACTATTCAA
 GATTCCAACTATGGTGGCAAGATCCCATTTGTGTGTTTTGCCCAAGGAGGTGCAAAAGACACTTTGAAAGCCAT
 CAATACCTCCATCAAAAATAAAATTCCTTGTGTGGTGGTGGAGGGCTCGGGCCGGATCGCTGATGTGATCGCTA
 GCTTGGTGGAGGTGGAGGATGCCCCGACATCTTCTGCGCTCAAGGAGAAGCTGGTGGCTTTTTACCCCGCAGG
 GTGTCCCGGCTGTCTGAGGAGGAGCTGAGAGTTGGATCAAATGGCTCAAAGAAATTCGAATGTTCTCACCT
 ATTAACAGTTATTAATAATGGAAGAAGCTGGGGATGAAATTTGTAGCAATGCCATCTCTACGCTCTATACAAG
 CCTTCAGCACCACTGAGCAABACAAGGTAACCTGGAATGGGCAGCTGAAGCTTCTGCTGGAGTGGAAACCACTG
 GACTTAGCCAATGATGAGATTTTACCAATGACCGCGGATGGGAGTCTGCTGACCTTCAAGAAGTCATGTTTAC
 GGCTCTCATAAAGGACAGACCCAGTTTGTCCGCTCTTCTGAGAGAATGGCTTGAACCTACGGAAGTTTCTCA
 CCCATGATGTCTCACTGAACCTCTTCTCCACCACTTCAGCACGCTTGTGTACCGGAATCTGCAGATCGCCAAG
 AATTCCTATAATGATGCGCTCTCACGTTTGTCTGGAAGCTGGTTGCGAACTTCCGAAGAGGCTTCCGGAAGGA
 AGACAGAAATGGCCGGGACGAGATGGACATAGAATCCACGACGTGTCTCTATTACTCGGCACCCCTGCAAG
 CTCTCTTCACTCTGGGCGATTCTTCAGATAAGAAGGAATCTCCAAAGTCATTTGGGAGCAGACCAAGGGCTGC
 ACTCTGGCAGCCCTGGGAGCCAGCAAGCTTCTGAAGACTCTGCCCAAGTGAAGAACGACATCAATGCTGCTGG
 GGAGTCCGAGGAGCTGGCTAATGATACGAGACCCGGGCTGTTGAGCTGTTCACTGAGTGTACAGCAGCGATG
 AASACTTGGCAGAACAGCTGCTGCTATTCCTGTGAAGCTTGGGGTGGAGCAACTGTCTGAGCTGGCGGTG
 GAGGCCACAGACCACTTTCCCGCCCGAGCTGGGCTCCAGAAATTTCTTTCTAAGCAATGATATGGAGAGAT
 TTCCCGAGACACCAGAAGCTGGAAGATTATCCTGTGTCTGTTTATTATACCCCTGGTGGGCTGTGGCTTTGTAT
 CATTTAGGAAGAAACCTGTGACAGCACAGAAGCTGCTTTGATATATGTGGCGTTCTTCACCTCCCCCTTC
 GTGGTCTTCTCCTGGAATGTGGCTCTTCTACATCGCTTCTCTCTGCTGTTTGGCTACCTGCTGCTCATGGATT
 CCTTCGGTGGCACACCCCCCGAGCTGGTCTGTACTCGCTGGTCTTTGTCTCTTCTGTGATGAAGTGAGAC
 AGTGGTACGTAAATGGGCTGAATTATTTACTGACCTGTGGAATGTGATGGACAGCTGGGGCTTTTTTACTTC
 ATAGCAGGAATGTATTTCCGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGAAGAGTCATTTTCTGTCT
 GGACTACATTTATTTCACTCTAAGATGATCCACATTTTACTGTAAGCAGAACTTAGGACCCAAGATTATAA
 TGCTGCAGAGGATGCTGATCGATGTGTCTTCTCTCTCTCTCTTGGCGTGTGGATGGTGGCTTTGGCGTG
 GCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTGGAGGTGGATATTCGGTTCGGTCTATCTACGAGCCCTA
 CCTGGCCATGTTCCGCCAGGTGCCAGTGAAGTGGATGGTACCACGTATGACTTTGCCCACTGCACCTTCACTG
 GGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGCCCGGTTCCCGAGTGGATCACCATC
 CCCCCTGGTGTGATCTACATGTTATCCACCAACATCTGCTGGTCAACCTGCTGGTGGCATGTTTGGCTACAC
 GGTGGGCACCGTCCAGGAGAACAAATGACCAGGTCTGGAAGTTCCAGAGTACTTCTGGTGCAGAGTACTGCA

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FIGURE 17B

GCGCGCTCAATATCCCCCTTCCCCCTTCATCCTCTTCCCTTACTTCTACATGGTGGTGAAGAAGTGCCTTCAAGTGT
 TGCTGCAAGGAGAAAAACATGGAGTCTTCTGTCTGCTGTTTCAAAAATGAAGACAATGAGACTCTGGCAATGGGA
 GGGTGTCTATGAAGGAAAACCTACCTTGTCAAGATCAACACAAAAGCCAAACGACACCTCAGAGGAAATGAGGCATC
 GATTTAGACAACCTGGATACAAAGCTTAATGATCTCBAAGGCTCTTCTGAAAGAGATTGCTAATAAAATCAAAATAA
 AACTGTATGAACTCTAATGGAGAAAAATCTAATATATGCAAGATCATATTAAGGAATGCTGATGAACAATTTT
 GCTATCGACTACTAAATGAGAGATTTTCAGACCCCTGGGTACATGGTGGATGATTTTAAATCACCCCTAGTGTGC
 TGAGACCTTGAGAATAAAGTGTGTGATTGGTTTTCATACTTGAAGACCGATATAAGGAGAGAAATTTCCCTTAT
 GTGTTTCTCCAGAATGGTGGCTGTTTCTCTGTGTCTCAATGCCCTGGGACTGGAGGTTGATAGTTTAACTGTG
 TTCTTACCGCCTGCTTTTCCCTTAATCTTATTTTGGTGAACATATATAGGAGAACATCTATCCCTATGAAT
 AAGAACCCTGGTCACTCTTACTCCTGTATTTGTTATTTTGTTCATTTCCAAATTCATTCTCTACTTTTCCCTTTTT
 TGTATTATGTGACTAATTAAGTTGGCATATTGTTAAAGTCTCTCRAATTAAGGCCAGATTCTAAAACATGCTGCA
 GCAAGAGGACCCCGCTCTCTTCAGGAAAAGTGTTTTCATTTCTCAGGATGCTTCTTACCTGTGAGGGAGGTGA
 CAAGGCAGTCTCTTGTCTCTTGGACTCACCCAGGCTCCTATTGAAGGAACCCACCCCATTCCTAAATATGTGA
 AAGTCGCCCCAAATGCAACCTTGAAAGGCACTACTGACTTTGTTCTTATTTGGATACCTCTTATTTATTTATTT
 TTCCATTAAAAATATAGCTGGCTATTATAGAAAATTTAGACCATACAGAGATGTAGAAAGAACATAAATTTGTC
 CCCATTACCTTAAGGTAACTACTGCTAACAAATTTCTGGATGGTTTTTCAAGTCTATTTTTTTCTATGTATGTC
 TCAATTCTCTTTCAAAATTTTACAGAATGTTATCATACTACATATATACTTTTTATGTAAGCTTTTTCACFTAG
 TATTTTATCBAATATGTTTTTATTATATTCATAGCCTTCTTAAACATTATATCAATRAATTCATAATAGGCAAC
 CTCTAGCGATTACCATAAATTTGCTCATGAAAGCTATCTCCAGTTGATCATTTGGGATGAGCATCTTTGTGCAT
 GAATCCTATTGCTGTATTTGGGAAAATTTTCCAAGGTTAGATTCCAATAAATATCTATTTATTTAATATTA
 AATATCGATTTATTTATTTAAACCATTATAAAGGCTTTTTCATAAATGTATAGCAATAGGAATTTAATCTTG
 AGCATAAGATATGAGTACATGAACCTGAACATTTAAATATAAATATTATATTTAACCCTAGTTTAAAGAAGAG
 TCAATATGCTTATTTAATATTTATGGATGGTGGGAGATCACTTGAGGTGAGGAGTTCGAGACCAGCCTGGCCA
 ACATGGCAAAACCACATCTCTACTAAAAATAAAAAAATTAGCTGGGTGTGGTGGTGCACCTCTGTAAATCCCAGC
 TACTCAGAAGGCTGAGGTACAAGAATTTGCTGGAACCTGGGAGGCGGAGGTTGCAGTGAACCAAGATTGCACCAC
 TGCACCTCCAGCCGGGGTGACAGAGTGAGACTCCGACTGAAATATAAATAAATAAATAAATAAATAAATAAATAA
 TAAATATTATGGATGGTGAAGGAATGGTATAGAAATTTGGAGAGTTATCTTACTGAACACCTGTAGTCCCAGCT
 TTCTCTGGAAGTGGTGGTATTTGAGCAGGATGTGCACAAGGCAATTTGAAATGCCCATAATTASTTTCTCAGCTT
 TGAATACACTATAAACTCAGTGGCTGAAGGAGGAAATTTTGAAGGAGCTACTAABAGATCTAATTTGAAAAA
 CTACAAAAGCATTAACATAAAAAAGTTTATTTTCTTTTGTCTGGGCAGTACTGAAAATAACTACTCACAACAT
 CACTATGTTTGAAGGAATTAACACAATAAAGATGCCCTTTTACTTAAACGCCAAGACAGAAAACCTGCCCCA
 ATACTGAGAAGCACTTGCATTAGAGAGGGAAGTGTAAATGTTTCAACCCAGTTCACTCTGGTGGATGTTTTT
 GCAGGTTACTCTGAGAATTTTGTCTATGAAAAATCATTTATTTTATGTAGTTTCAACAATAATGTATTGAACATA
 CTTCTAATCAAGGTGCTATGCTTGTGTATGGTACTAAATGTGTCTCTGTGTACTTTTGCACAACCTGAGAAATC
 CTGCGGCTTGGTTTAAATGAGTGTGTTTATGAAATAAATAATGGAGGAATTTGTCAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

[illegible]

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FIGURE 19

GCGGCGGGGSCGAGGTGAGGTGTTGGCACTGGAAGGGGTTCCGGGCTCGGGGGGCGGGGGGAAGCGGAGCGGAT
 GGGCCGCGCGCGGGCGCGAGGGGCGGATAAAAAGCCGTCGCGCTCGCGGAGTGGGCGGGAGGSGAGGGGGGTGTCC
 GAGGGCCACAAGAGTATGACGGGGCTGTACGAGCTGGTGTGGCGGGTGTCTGCACGGCTGTCTGTCTGCACCG
 CAGGCTCACCTCCTGGGCTCCGGCTTCGGTTTCGGCACTGGAACTGGATCTGGCGGGCGCTGTCCGGCGCGGGCT
 CTGCGCGGGCTCTAGCGCGGCTCGGGCTTCACGCTCCCGCAAGCCCCGGCAGTCCGSCAGGAACCGCGTCACCAC
 CCGCACCCGCGCGGGGGGTGCTGCTGGCAGCCGACACCCACCGGATGCGCTGGGCGCGGAGCGGTGCTTCCTT
 GGAGAAGCTGCCCTGTGCTATATGGGCTTGGTGATCACCGAGGTGGAGCAGGAACCCAGCTTCFUGGACATCGGA
 GCTCGTGGTGTGGTGTATGGCCGTGGGCATCTCTACATFAGCGTCTACGACCACCAAGGTATTTTCAAAGA
 AATAATTCAGATTGATGGATGAAATTTTAAACACACAGCAAGAACTTCTGGGCTAGATTGTTCAAATATCTC
 ACCAGAATTTGCAAAATAGTAATGACAAAGATGATCAAGTTTAAATTTGCCATTGGGCAGTGAAGGTGCTGTCTC
 CGGAAGATGGAAAGCAGATATTGTAAAGAGCTGCTCAGGACTTTTGCCAGTTAGTAGCCAGAGCAAGGAGAG
 CCCACAGATTTGGATGTAGATACGTTAGCCAGTTTACTTTAGTTCAAATGGTTGTCTGTATCTGATTTAGTATT
 GAAGTTCCGTCCTGTGGACAGCACATFAGGCTTTCTCCCTGGCACATCAGATTGACTGAGATTSTCTCTTTGC
 CTTCCACCTAARACATCAGTTATGAGGACTTTTTCTCTGCCCTTCGCTCAATATGCAGGCTGTGAACAGCGTCTG
 GCAAGTACGTTGCTATTGCTTGCATAATTTGATTTGAGGCTTGTGGAGGAAGGAACCAAGTACTCTGATGTT
 TACAAAGCACTATGAAACCTGTACACACCTATGAAACCTGTACACACCTAGTTCAATCTCATAATCTCATAATTTA
 TCAACAAACACAAAGAGTGTCTTACTTTGAGAGTGAAGTGTGTGCGGTGTGTGCGTGACACAGTGTGCACSTTTGT
 ATGTGTGGAATAAACATAAATGGGACGTTGTTGGAGGAAGGAATAACATAGACCTACAACCTTTGAGCATATAGC
 AGTGATGTTTTAGGAAGTGAATGTCAACCTTAATAAGTCTTCAGCCAGCTACTTCCCTGTTTTCTGGGGGA
 GAAGGGGGCTGATTAGAACCTGTTCTGGTGTGTTTGGCGGGAGGGGAATAAATTTTGTTCAGTCTCTCTTAGT
 GACCAACCTTTAATTTTAGGAATAACATATTGACTTACTGAACTGAAGCATTCTGAGTTGAAGAGGAGCCCCAG
 AGGAAGGAGTTCGTGTTGCTCACATGTTAAAGCTTGTCTACCTTCAGAGCAGAGGGAATACCTATCTTCAG
 ATATCCGCCCCATTTCATCTCTTCATTTATAGTCAAAACAGTGTGACTTGAGAGTGTGTGCTGTGCTGTATTC
 TGGCTTATGAAGATTATTTGAAAAAGAACTCTTACTACATTTGAAATGCAGACTTTTAAAAATTTAATATTGGA
 TTAGGCACTCAAAAAACCAACAAAGCATAAAGGTCAAGTAACTTTAATCTTAAAGTAAGGTTGGAAAACTCA
 TTATAAATGGAAGAAAGTTTTGATTTCTTTTTTGTGTTGATGGGCACTATGCCATATTATCAAAAGTTGGT
 TTAATAAATACTTCCATCACTATTTTTTAAATTAACATTTGAGGGAAGTTACCAAGGCAGCTTTTTTCC
 TCARAAGTAACCTGTTCTCTTGGAAACAGCACATTTTAGGGGCATGGTTAATACCTGAGATTTTACTCAGTA
 AACCTGATGGTTACCGTGTGTGAAAAATCTTTAAGTAGGATTTGAAGGCTCTGTGGGGAATATAATGTTACCAA
 AGCCTATAAAAAATRAATTTTACATGTTCTTTTTTATGACAGAGAGCAGCACTGGTTCTGTTATTTTTTAAATG
 AATAACTGATTTCTTGACAGGTGTTTAGTATTTCTTCCCTCACTGCTGATTTCTTGGATAGAAACCTTTCTTTAT
 ATTTGATAGACTGTTTTGAGAAACCTCTTATCAACCACTGTACAAATAGTTATCTAAACTGTACATTTAGAATG
 GAGCAGTTTAATACTAGATCTCAGAAATTTGAAAAATAGCAAGAAGACTGGATTTGSAAGCATGGTCTACAA
 TTGCTTGTCAATCTGAAGCTATGAAGAATAAATGTTTCACTTTGGATTATGAAACCCCTTATGATTTTTTA
 AAACACACTTGAATAAAAAATGATTGAACATAAATTTTGGTCCGGTGACATCATTTTGCCTGCTAGCCCCATTA
 TACATTTGTAAGTCTTTTTGTTTTAATTTATTACTGAGAGTTTCTGTGAAGCTACAGCATATCTAANTCAGAGAA
 TTTCTGATTTGTTTCTTATCTGTGATTATGTTATTTAAGGCATTTGTAGTGCAGCTTAAGACTGAATTTAE
 GCTTTTTGTAAACATGATCGGTGTAAATGTCTTATAAACATTTCTGGAGTATGTATACTTTAATGAATGAATTT
 TATGGACCTGATTAATAAAGGCAATTTAATCTTTGTTAAAGTGAAGTTAGTGGAAATAAATTACCTACTGGAA
 TATAGTCCAAAGTCACTAAAGSTTTAATATTTGCATTTTGTGCTTTTATTTTCTCCTTCCATTCATAATTTATAT
 ACTTGAAGGTACATCTGTAGCCTATGACTTGAGTCTCTTGAACCTTCTAGGAAGAGGCAACTACAACTACTAG
 GATTTCTGATTTTCAATATAGGCATTCAGAACTCTCTCTTTACGAGTTCACTGCTAGTATAATCTCCACAAC
 TGAATGGCCTTGGTGTCTGTAAATGCTGCCAAATCATCACAGCTGTACGTCATCAAGGCTCCCTTTGCAC
 TCCCAAGAAGAAGTGTTCATTTAAACAAAGGTGTATGTCTTTATTTGTATTGGAAATATTGTCTTTAAATTTG
 TTTCTTGTGACACTTCCCACAATGGAAAAATTACCAATTAACCTGTTTTATGGATGGCAGCTTGGAGCATA
 GCAAGAAATTTGGAGGATTTGAATTCATTTCCAGTTCTCATTCGCTTTGTTTTCTTAAACTATAAATTTGGT
 TACTGTTATAAAGTTTAAAGGTGTTTTAATATGAATAGCAATTCGGAATATTGTGACTAACCGTTAAGAA
 TGCTGTCTTTGAGAGGAAGGTGTTAATATTAATCAACAGTGCCAAATACACTGTGCATATCTACAATTTAA
 TCTTTGAATGTTTGTACTGGATAGCTCCCTCCTCCTCTGTGTGATGGTACCATGCATAGACTCAATCAAT
 CTTTGTGATGTTTTGTATGGACTTTGACAACTGTAACTAATGTGTAAAGCAAGTTTTTATGATTAAGGAATCA
 AATTTATTAATTTTATTTATTAAGTTGAACTTAACATGTATAAAACAAAAACAATAAATAAATAAATATT
 TTCATTGACTATAAAAAAAGGCCACCGCTCCGCG

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FIGURE 20

GAGGTGAGGTGTTGGCAGTGGAAAGGGGTTCCGGGCTCCGGGGGCGGGGGGACGGGGAGCGATGCCCCGGCCGG
CCSCAGGGGGCGGATAAAAAAGCCCTCGCGCTGCCGGGASTGGGCGGGAGGGAGAGGGGGTGTCCGAGGGGCCACAAG
AGTATGACGGGGGCTGTACGAGCTGGTGTGGCGGGGTGCTGCACGCGCTGCTCTGTCTGCACCGCACGCTCACCTC
CTGGCTCCCGGTTCCGGTTCGGCACCTGGAACTGGATCTGGCGCGCTGCTGCTGCCGCGCCGCTCTGCCGCGGTCC
TAGCGCCGCTCGGCTTCACGCTCCGCAAGCCCCCGGAGTCGGGTAGGAACCGCCGTCACCCACCGGCACCCGCGC
GGGGGGTCTGCTGGCTGGCAGCCGACACCCAGGATCGGCTGGCGCGCGGACGCTGCTTCTTGGAGAAGCTGCC
TGTGCATATGGGCTTGGTGATCACCGAGGTGGAGCAGGAACCCAGCTTCTCGGACATCGCGAGCCTCTGTGGTGT
GGTGTATGGCCGTGGGCATCTCCTACATTAGCGCTCTACGACCACCAAGGTATTTTCAAAAGAAATAATTCAGA
TTGATGGAAGAAATTTTAAACAACAGCAAGAACTTCTGGGCTTAGATTGTTCAAAATACTCACCAGAAATTCG
AAATAGTAATGACAAAGATGATCAAGTTTTAAATTGCCATTTGGCAGTGAAGGTGCTGCTCTCCGGAAGATGGAA
AAGCAGTATTTGTAAGAGCTGCTCAGGACTTTTGCCAGTTAGTAGCCAGAAAGCAGAGACCCACAGATTTG
GATGTAGATACGTTAGCCAGTTTACTTAGTTCAATGGTTGTCCTGATCCTGATTAGTATTGAAGTTGCGTCC
TGTGGACAGCACATTAGGCTTTCTTCCCTGGCACATCAGATTGACTGAGATTGTCTCTTTGCCCTTCCCACCTAA
ACATCASTTATGAGGACTTTTTCTCTGCCCTTCGTCAATATGCAGCCTGTGAACAGCGTCTCGGAAAGTAGTGG
TCATTGGTTGCA

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FIGURE 21

GGGGGGGGGAACCAAGCTTCACCGGCTGGCTCCGGGTGACAGCCGCGCGCTCCGCCAGGATCTGAGTGATGAG
ACGCTGTCCTCCCACTGAGTGTGCCCCACAGCAGCAGGTGTGTGASCATGGGGCTGAGAAAGCTGGACCCGACCCAAAGGG
CTGGCAGAAATGGGGCGCTGGGTGATTCTTAGGCATTGGCGGCAGCAAGCAGGAGAGGGCCGACGCTTCTGGAG
CAGAGCCGAGACGAAGCASTTCTGGAGTGCCCTGAACCGGCCCTTGAGCCCTACCCGCTTGGCCCACTATGGTCC
AGAGGCTGTGGGTGAGCCGCTTCTGCTGCGGCACCCGGAAGCCACAGCTCTTGTCTGGTCAACCTGCTAACTTTGGC
CTGGAGGTGTGTTTGGCCGACAGGCATCAGCTATGTGCGCGCTCTGCTGCTGGAAGTGGGGGTAGGAGCAAGT
CATGACCATGTGCTGCTGGGCATTGGTCCAGTCTGGGCTGGTCTGTGTCGCGCTCTAGGCTCAGCCAGTGAUC
CTGGGCTGGAGCCGCTATGGCGGCGCGCGGCTTCTCATCTGGCACTGTCTTGGGCATCTGCTGAGCCTCTTT
CTCATCCCAAGGCGCGCTGAGCTAGCAGGGCTGCTGTGCGCGGATCCCAAGGCCCTGGAGCTGGGACTGCTCAT
CCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCT
TCCGGGACCCGGACCACTGTGCGCCAGGCTACTCTGTCTATGCCCTCATGATCACTCTGGGGCTGCTGGG
TACCTCTCGGCTGCCATTGACTGGGACCACTGAGTCCCTGGCCCTACCTGGCCACCCAGGAGAGTGCCTCTT
TGGGCTGCTCACCCTCATCTCTCCTCAGCTGGGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCCAGGCTGGGC
CCACCGAGCCAGCAGCAAGGGCTGTGCGCGGCTCTCCTTGTGCGCCACTGCTGTCCATGCCGGGCCGCTTGGCT
TTCCGGAAGCTGGGCGCGCTGCTTCCCGGCTGACCCAGCTGTGCTGCCGATGCCCGGACCGCTGCGCGCGCT
CTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCAAGCTGTTTTACAGGATTTGCTGGGCGAGG
GGCTGTACAGGGCTGCCCAGAGCTGAGCGCGGCAACCGAGGCCCGGAGACACTATGATGAAGCGCTTCGGATG
GGCAGCCTGGGGCTGCTCCTGCACTGCGCGCATCTCCCTGGTCTTCTCTCTGCTCATGGACCGCTGGTGCAGCG
ATTCCGCACTCGAGCACTATTTGGCCAGTGTGGCACTTTCCCTTGGCTGCGGCTGCGGCTGCCCATGCTGCTGCC
ACAGTGTGGCTGTGTCAGCACTTCAGCGCGGCTCACCAGGCTTCACTTCTCAGCCCTGCAGATCCTGCCCTAC
ACACTGGCTCCTCTACCAACCGGGAGAGCAGCTGTTCTGCCCAATACCGAGGGGACACTGAGAGTCTAG
CAGTGAGGACAGCCTGATGACAGCTTCCGCGCAGGCCCTAGCCTGGAGCTCCCTTCCCTAATGGACAGCTGG
GTGCTGGAGGCAAGTGGGCTGCTCCACCTCCACCGCGCTCTGCGGGGCCCTGCTGCTGTGATGTCTCCCTAGCT
GTGGTGGTGGGTGAGCCCAAGGCGAGGCGAGGTGGTTCCGGGCGGGGCACTGCGCTGGAGCTGCGCATCCTGGA
TAGTGCCTTCTGCTGCTCCAGCTGGCGGCTGCTTCTGTTATGGCTCCATTTGTCCAGCTCAGCAGTCTGTCA
TGCTCCTATATGGCTGCTGCGCGAGGCTGGGTCTGCTGCTGCTTACTTTGCTACACAGCTAGTATTTGACAAG
AGCGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGTGCGAGGGCTGCTCCTCACTGGGTCCCA
GCTCCCCGCTCCTGTGTAGCCCCATGGGCTGCGCGGCTGGGCGGCACTTTCTGTTGCTGCCAAAGTATGCTGGC
TCTCTGCTGCCACCTGTGCTGCTGAGGTGCGTAGCTCAGCAGCTGGGGCTGGGGCTCCTCTCTCTCTCTCC
CCAGTCTCTAGGGCTGCTGACTGGAGGCTTCCAGGGGTTTCACTCTGAGCTATACAGGAGGCCAGAG
GGCTCCACTGCACTGGAATGTGGGACTCTGAGGTGATTAACCAAGCTCAGGGTTACAGCTAGCCTCCTAGT
TGAGACACACTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACTGGTTCCCATCTCTAAGGCCCTT
AACCTGCAGCTTGGTTAATGTAGCTCTTGCATGGAGTCTTAGGATGAACACCTCCTCCTGGGATTTGAAC
ATATGAAGTATTTGTAGGGGAAGAGTCTGAGGGGCAACACAGAGCAAGCTCCCTCAGCCCCACAGCAC
TGCTTTTTGCTGATCCACCCCCCTCTTACCTTTTATCAGGATGTGGCTGTGTGCTCTGTGTTGCCATCAC
GAGACACAGGCATTTAAATATTTAACTTATTTATTAACAAAGTAGAAGGAATCCATTGCTAGCTTTTCTGTG
TTGTTGCTCTAATATTTGGGTAGGTGGGGATCCCCAACATCAGGTCCCTGAGATAGCTGGTCTATTGGGCTG
ATCATTTCCAGAATCTTCTCTCTCTGGGCTGCGCCCCCAAAATGCCCTAACCCAGGACCTTGGAAATCTTACT
CATCCCAAAATGATATTTCCAAATGCTGTTACCAAGGTTAGGGTGTGAAGGAAGGTAGAGGCTGGGGCTTCA
GTCTCAAGGGCTTCCCTAACCCACCGCTGTTCTCTTGGGCCAGCCTGGTTCCCCCACTTCCCTCCTACT
CTCTCTAGGACTGGGCTGATGAAGGCCTGCCCAAAATTTCCCTAOCCTCACTTCCCTAOCCTAOCCTAOCCT
CCCCACAGCTCCCAACCTGTTTGGAGCTACTGCAGGACAGAGACAAAGTGGGTTTCCCAAGCCTTTG
TCCATCTCAGCCCCCAGAGTATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCCCTGCTGAG
CTAAGGAGGCTTATCTCTCAGGGGGGTTAAGTGCGGTTTGCAATAATGTGCTTATTTATTTAGCGGGT
GAATATTTTATCTGTAAGTGAGCAATCAGATATAATGTTTATGGTGACAAATTAAGCCTTCTTATATGTTT

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FIGURE 22

AACAAAAGCTGGAGCTCCACCGGGTGGCGGGCGCTCTAGCCCTTGGTTTCGGCCCACTCTGAAGGTTCCAGAA
 TCGATAGTGAATTTCGTGGGGAAGCCAGCCATGGCTCTGCGGAGGCTGGGGCCCGCGCTGCTGCTGCTGCGGCT
 GCTCGCCGCCGTGGGAAGAAACGCTAATGGACTCCACTACAGCACTGCTGAGCTGGGCTGGATGGTGCATCCTC
 CATCAGGGTGGGAAGAGGTGAGTGGCTACGATGAGAACATGAACACGATCCGACGTAACAGGTGTGCAACGTG
 TTTGAGTCAAGCCAGAACCACTGGCTACGAGCAAGTTTATCCGGCGCCGTGGCGCCACCGCATCCAGCTGGA
 GATGAAGTTTTTCGGTGGCTGACTGCAGCAGCATCCCCAGCGTGCCTGGCTCCTGCAAGGAGACCTTCAACCTCT
 ATTACTATGAGGCTGACTTTGACTGCGCCACCAAGACCTTCCCAACTGGATGGAGAATCCATGGGTGAAGGTG
 GATACCATTTGCAGCCGACGAGAGCTTCTCCAGGTGGACCTGGGTGGCGCGCTCATGAAAATCAACACCGAGGT
 GCGGAGCTTCGGACCTGTGTCCCGCAGCGGCTTCTACCTGGCTTCCAGGACTATGGCGGCTGCATGTCCCTCA
 TCGCCGTGGGTGTCTTCTACCGCAAGTGGCCCCGCATCATCCAGAAATGGCGCATCTTCCAGGAACCTGTGG
 GGGCTGGAGAGCACATCGCTGGTGGCTGCCCGGGGAGCTGCATCGCCAATGCGGAAGAGGTGGATGTACCAT
 CAAGCTCTACTGTAAACGGGACGGGAGTGGCTGGTGGTGGCTCGGGCGCTGCATGTGCBAAGCAGGCTTCGAGG
 CCGTTGGAATGGCAACCTCTGCGGAGCTTGTCCATCTGGGACTTTCAAGGCCAACCAGGGGATGAGGCTGT
 ACCACTGTCCCATCAACAGCCGAGACCTTCTGAAGGGGCCACCAACTGTGTGCGCGCAATGGCTACTACAG
 AGCAGACCTGGACCCCTGGACATGCCCTGCCAACCATCCCTTCGGCGCCCGAGGCTGTGATTTCCAGTGTCA
 ATGAGACCTTCCCTCATGTGGAGTGGACCCCTCCCGCGACTCCGAGGCGCGAGAGACCTCGTCTACACATC
 ATCTGCBAAGAGCTGTGGCTCGGGCGGGGTGGCTGCACCCGCTGGGGGACAAATGTACAGTACGCAACCCAGCA
 GCTAGGCTGACCGAGCCACCGATTTACATCACTGACCTGCTGGCCACACCCAGTACACCTTCGAGATCCAGG
 CTGTGAACGGCTTACTGACCAAGAGCCCTTCTCGGCTCAGTTCCGCTCTGTGAACATCAACACCAACAGGCA
 GCTCCATCGGGCAGTGTCCATCATCATCAGGTGAGCCGCAACCTGGACAGCATTACCTGTGTGGTCCAGCC
 AGCAGAGCCCAATGGCGTGTCTCTGGACTATGAGCTGCAGTACTATGAGAAGGAGCTCAGTGAATACAAGCCCA
 CAGCCATAAAAAGCCCCACCAACACGGTCAACGCTGCAGGGCCCTCAAAGCCGGCGCCATCTATGTCTTCCAGGT
 CGGGCAGCGACCGTGGCAGGCTACGGGGGCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAAGCCGAGTA
 CCAGACAAGCATCCAGGAGAATTTGCCACTCATCAFGGCTCCTCGGCCCTGGCTTCTTCTCATTTGCTG
 TGGTTGTCTATCGCCATCTGTGTAAACAGAAGACGGGGCTTIGAGCGTGTGACTGGGAGTACACGGACAAGCTG
 CAACACTACACCAAGTGGCCACATGACCCCGAGGCTGARGATCTACATCGATCCTTTCACTTACGAGGACCCCAA
 GGAGGAGTSCGGAGTTTCCCAAGGAAATGACATCTCTGTGTCAAAATGAGCAGGTGATCGGAGCGGGG
 AGTTTGGCGAGGTCTGCAGTGGCCACCTGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAGAGCTC
 AAGTGGGCTACACGGAGAAGCAGCGCCGGGACTTCTGAGCGAAGCCCTCCATCATGGGCCAGTTCGACCATCC
 CAAAGTCATCCACCTGGAGGGTGTCTGTGACCAAGAGACCACTGTGATGATCATCACCAGTTTCTGAGAGATG
 GCTCCCTGGACTCTTTCTCCGGCAAAACGATGGGCASTTCCAGTTCATCCAGCTGGTGGGCTGCTTCCGGG
 ATCGCAGCTGGCATGAAGTACCTGGCAGACATGAATATTTTCACTTACCTGAGCTGGCTGGCCGCAACATCTCTGT
 CAACAGCAACCTGGTCTGCAAGGTGTGGGACTTTGGGCTCTCAGCTTTCTAGAGGACGATACCTCAGACCCCA
 CCTACACCAAGTSCCTGGCGGAAAGATCCCATCCGCTGGACAGCCCCGGAAGCCATODAGTACCGGAATTC
 ACCTCGGCCAGTGATGTGTGAGCTACGGCAATTTCTATGTGGGAGGTGATGTCTATGGGGAGCGGCCCTACTG
 GGACATGACCAACAGGATGTAAATCAATGCCATTGAGCAGGACTATCGGCTGCCACCGGCCATGGACTGCCCGA
 GCGCCCTGCACCAATCATCTCTGGACTGTTGGCAGAGGACGCGCAACACCGGCCCAAGTTCCGGCAATTTGT
 AACACGCTAGACAGATGATCCGCAATCCCAACAGCCTCAAAGCCATGGCGGCCCTCTCTCTGGCATCAACT
 GCGGCTCTGGACCGCAGATCCCGACTACACAGCTTTAACACGCTGGACGAGTGGCTGGAGGCCATCAAGA
 TGGGGCAGTACAAGGAGAGCTTCCGCAATGGCGGCTTCACTCTCTTGGAGTGTGTCTCAGATGATGATGGAG
 GACATTTCTCGGGTTGGGCTCACTTTGGCTGGCCACCAAAAAAATCTGAACAGTATCCAGGTGATGGCGGC
 GCAGATGAACAGATTCACTCTGTGGAGTTTGAATTCACCTTCCCTGGCTCACCTCTTCTCTCAAGCCCCCG
 CCCCCTGCGCCCACTGCGGCCCTCTGTGCTCTACTGCAAGGSCAGCCACTGSCCAGGAGGCCAGG
 GCCACGGGAAGAACCAAGCGGTGCCAGCCAGAGAGCTCACCAGAAACATGCAACTCAAACGACGGAAAAAA
 AAGGGGAATGGAAAAAAGAAACAGATCTGGGAGGGGGGGGAAATACAAGGAATATTTTTTAAAGAGGAT
 CTCTAAGGAAAGCAATGACTGTTCTTGGGGGATAAAAAGGGCTTGGGAGATTCTATGCGATGTGTCCATC
 GGAGACAAAAGCAATTTCTCTCAACTCCCTCTGGGAAGGTGACCTGGCCAGAGCCAAAGAAACATTTTCAGAAA
 AACAAATGTGAAGGGGAGAGACAGGGGGCGCCCTTGGCTCCTGTCTCTGCTGCTCTCTAGGCTCTACTCAACA
 ACCAAGCGCTGGAGGACGGGACAGATGGACAGACAGCCACCTGAGAACCCCTCTGGGAAATCTATCTCTGTC
 CACCACTGGGCAACAGGAATTTTTCTGTCTTTGGAGAGATTTTTAGAACTCCAATGAAGACACTGTTTC
 TCTGTGGCTCACAGGCTGAAAGGGGCTTTGTCTCTCTGGCTCAGGAGAACGCGGGGACCCAG

[illegible]

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FIGURE 24

CCGCCAGCTCCCTTCGGGCAATGAACTTCTCCACCAGCAGCAGCAGCTTCGCCCTACGACCGGGAGTTCCTCCGGCAC
CCTGCCCCGGCTTCCTCATCGTGGCCGAGATCGTTCTGGGGCTGCTGGTATGGACCGCTTATTGCTGGAACTGAGT
ACTTCGCGGTCCCCGCATTTGGCTGGGTCAFGTTTGTAGCTGTATTTTACTGGGTCCCTCACCSTCTTCTTCCTC
ATTATCTACATAACAATGACCTACACCAGGATTCCCCAGGTGCCCTGGACAACAGTGGGCTGTGCTTTTACGG
CAGTGCCTTCGTCTTGTACCTCTCTGCCGCTGTTGTAGATGCACTCTCCCTCTCCCTGAGAGGGACAGTCACA
ACTTCAACAGCTGGGCGGGCTCATCGTTCTTTGCTTCCTGGTCAACATCTGCTACGCTGGAAATACATAATTC
AGTTTTATAGCATGGAGATCCAGGACCATACAGTGAATTTACCATTTTGATAATTTAAAGGAAAAAAAAGGAAG
ACTCTCACTGTAAAAACAGCTGTAGGTATAATGTATATTCAGAGAAATGTATTTAACTAATTAATGTFTTTT
ATATTCCTTAAATTTGCTCACAAATGTGGTTTGTACAAATTAAGTGGATACTTATTTGCAAAGTGTGTAGCT
TATAATGAACCTCTTAAGTATCTTATTATGTATTAATGTCCTCATAGATCATATTTCTTAGACAATGTTTAAA
TAGATAAATTGCTAAATATTGAGAAATGTGTCAAGTTTGTAAACCTAACTTTTAAGATGCCAGATTCTTTTTTGAT
TAAATGTTGCBAATCCCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 25

GCCCTTGGCAATGGAACCTTCTCCACCAGCAGCAGCAGCTTCGCTACGACCGGGAGTTCCCTCCGCACCCCTGCCCC
GCTTCCTCATCGTGGCCGAGATCGTTCTGGGGCTGCTGGTATGGACGCTTATGCTGGAACTGAGTACTTCCGG
GTCCCCGCAATTGGCTGGGTCAATGTTGTAGCTGTATTTTACTGGGTCCTCACCGTCTTCTTCCTCAATTATCTA
CATAACAATGACCTACACCAGGATTCGCCAGGTGCCCTGGACAACAGTGGGGCTGTGCTTTAACGGCACTGCCF
TCGTCTTGTACCTCTCTGCCGCTGTTGTAGATGCATCTTCCGTCTCCCTGAGAGGGACASTCACAACCTTCAAC
AGCTGGGGCGGCTCATCGTTCTTTGCCCTTCCTGGTCACCATCTGCTACGCTGGAAATACATATTTCACTTTTAT
AGCATGGAGATCCAGGACCATACAGTGAATTTACCAAAGGGC

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FIGURE 26

GGUCCCTGCCCTGAAGGCTGGTCACTTGCAGAGGTAACCTCCCTCTTTGACTTCTGGCCAGSSTTTGTGCTGAG
CTGGCTTCAGCCGCTCTCAGCCTCGCTCCGGGCACGTCGSSCAGCCTCGGGCCCTCCTGCCTSCAGGATCATGC
CCACCACCCTGGACGATGTCTGGAGCATGGAGGGGAGTTTCACTTTTCCAGAAGCAATGTTTTCTCTTG
GCTCTACTCTGGCTACCTTCGCGCCCATCTACCTGGGCATCGTCTTCTGGGCTTCACCCCTGACCAACGCTG
CCGGAGCCCCGGAGTGGCCGAGCTGAGTCTGCGCTGCGGCTGGAGTCTTCAGAGGAACTGAACACACGGTGC
CGGGCCCAAGGACCTGCGGGCGAAGCTCCCCCAAGACAGTGTAGGCGCTACGAGGTGGACTGGAAACCAGACACC
TTTGACTGCGTGGACCCCCCTGGCCAGCCTGGACACCAACAGGAGCCGCTGCCACTGGGGCCCTGCCGGAGCGG
CTGGGTGTACGAGACGCTGGCTCGTCCATCGTCCAGGASTTTAACCCTGGTATGTGCCAACTCCTGGATGTGG
ACCTATTCAGTCACTAGTGAATGTAGGATTCTTTATTGGCTCTATGAGTATCGGCTACATAGCAGACAGTTT
GGCCGTAAGCTCTGCTCCTAACTACAGTCTCTATAAATGCTGCAGCTGGAGTCTCATGGCCATTTCCCAAC
CTATACGTGGATCTTAATTTTTCCCTTAATCCAAGGACTGGTCAGCAAGCAGGCTGGTTAATAGGCTACATCC
TGATTACAGAAATTTGTTGGGCGGAGATATCGGAGAACAGTGGGGATTTTTTACCAAGTGGCTATACAGTTGGG
CTCCTGGTCTAGCTGGGGTGGCTTAAGCACTTCTCTACTGGAGGTGGTTGGAGTTCACAGTTGCTCTGCCAA
CTTCTTCTTCTGCTCTATTACTGGTGCATACCTGAGTCTCCAGGTGGCTGATCTCCAGAAATAGAAATGCTG
AAGCCATGAGAACTCATTAAGCACATCGCAAGAAATAGAAATCTCTACCCGCTCCCTTCAGCGCCTGAGA
CTTGAAGAGGAACTGGCAAGAAATTGAACCTTCTCATTTCTGACTTGGTCAGAACTCCTCAGATAAGGAAACA
TACTATGATATGTATGTACAACTGGTTACAGAGCTCTGTGCTCTACCAGGGCTCATCATGCACATGGGCTTG
CAGGTGACATATCTAAGTGGATTTCTTCTACTCTGGCTGGTTGAATTCAGAGTGGCTTCATGATCATCTC
ACCATGACCGCATCGGACGCGCTTACCCCTGGGGCTGCATCAATATGTTTCAGGGGCGACCTGCTCTGGCTC
AGTTTTATACCTGGTGTCTACAATGGCTAAATTTATTTCTCATGCTTGGGAAGATGGGGATCACAAATGG
CCTATGAGATAGTCTGCCCTGGTCAATGCTGAGCTGTACCCACATTCATTAGGAATCTTGGCGTCCACATCTGT
TCCTCAATGTGTGACATTGGTGGCATCATCACGCCATTCCTGGTCTACCGGCTCACTAACATCTGGCTTGAGCT
CCCGCTGATGGTTTTCCGGCTACTTGGCTTGGTTGCTGGAGTCTGGTGGCTGTTGCTTCCAGAACTAAAGGGA
AAGCTTTGCCCTGAGACCATCGAGGAGCCGAAATATSCAAAGACCAAGAAAAAATGAAGAAASATGATTTAC
CTCCAGTTCAGAACTAGACATTCATTTGAACTAAGAGAGAGACCGTTGCTGCTGTATGACCTAGCTTTGA
TGGCAGCAAGACCAAAAGTAGAAATCCCTGCACTCATCAAGCCCATACAACCTCAACCAACCTACCCCTGA
GCCCTATCAACCTAGGTCTACAGCCAGTGGAGTCTATTGTACACTGTGGAAAAATACCCATGGGACCGATCCT
GCCAAATTTCTCCAGCTCACTTTATTCTCAGCATTCCTAGGACATTTGGACATTTGTTTTCTGGAGGGTTTTTTT
TCCGATCTTTGTATTTTTTAAATTTGATTCTTTCTTTGCAATGCTAGCAACCAGAAATACATAGGGGAATCT
GGGCTAGGCAAAANAAAAATAGAAAAAGTGTGAAAAACAGTAAAGTTGGGAGGGAGCATCTATTTTCTTAAAGAA
ATAAACACUNAAAAACAAAAA

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FIGURE 27

GCCCTTCTCCTGCCCTGCAGGATC**ATG**CCCCACCACCGTGGACGATGTCTCTGGAGCATGGAGGGGAGTTTCACTTT
 TTCCAGBAGCRAATGTTTTTCTCTTGGCTCTGCTCTCGGCTACCTTCGGCGCCCATCTACGTGGGCATGCTCTT
 CCTGGGCTTCACCCCCTGACCACCGCTGCCCCGAGCCCCGGAGTGGCCGAGCTGAGTCTGCGCTSCGGCTGGAGTC
 CTGCAGAGGAACCTGAACCTACACGGTSCCGGSCCCAGGACCTGCGGGCGAAGCCTCCCCAAGACAGTGTAGSCGC
 TACGAGGTGGACTGGAACAGAGCACCTTCGACTGCGTGGACCCCTGGCCAGCCTGGACACCAACAGGAGCCG
 CCTGCCACTGGGCCCCCTGCCGGGACGGCTGGGTGTACGAGACGGCTGGCTCTCTCCATCGTCACCGAGTTTAAAC
 TGGTATGTGCCAACTCCTGGATGTTGGACCTATTCAGTTCATCAGTGAATGTAGGATTCTTTATTGGCTCTATG
 AGTATCGGCTACATAGCAGACAGGTTTGGCCGTAAGCTCTGCCCTCCTAACTACAGTCCTCATAAATGCTSCAGC
 TGGAGTTCTCATGGCCATTTCGCCAACCTATACGTGGATGTTAATTTTTTCGCTTAATCCAAGGACTGGTCAGCA
 AAGCAGGCTGGTTAATAGGCTACATCCTGAATACAGAATTTGTTGGGCGAGATATCGGAGAACAGTGGGGATT
 TTTTACCAAGTTGCCATATACAGTTGGGCTCCTGGTGTAGCTGGGGTGGCTTACGCACTTCCTCACTGGAGGTG
 GTTGCAGTTACAGTTTCTCTGCCCAACTTCTTCTTCTTGTCTATTACTGGTGCATACCTGAGTCTCCCAGGT
 GGCTGATCTCCAGAATAAGAATGCTGAAGCCATGAGAAATCATTAAGCACATCGCRAAGGAAAAATGGAAATCT
 CTACCCGCTTCCCTTCAGCGCTGAGACTTGAAGAGGAACTGGCAAGAAATGGAACCTTCATTTCCTGACTT
 GGTGAGAACTCCTCAGATAAGGAAACATACTATGATATGATGTACAACTGGTTCACGAGCTCTGTGCTCTACC
 AGGGCCTCATCATGCACATGGGCTTGCAGGTGACAATATCTACCTGGATTTCTTCTACTCTGCCCTGGTTGAA
 TTCCCAGCTGCCTTCATGATCATCCTCACCATCGACCCCATCGGACGCGCTTACCCTTGGGCTGCATCAAATAT
 GGTGACAGGGGACGCTGTCTGGCCTCAGTTTTTATACCTGGTGTATCTACAATGGCTAAAAATTAATATCTCAT
 GCTTGGGAAGAAATGGGGATCACAATGGGCTATGAGATAGTCTGCCCTGGTCAATGCTGAGCTGTACCCACATTG
 AATTAGGAATCTTGGCGTCCACATCTGTTCCCTCAATGTGTGACATTGGTGGCATCATCACGCCATTTCCTGGTCTA
 CCGGCTCACTAACATCTGGCTTGAGCTCCCGCTGATGGTTTTTCGGCTGCTTGGCTTGGTGTGCTGGAGGTCTGG
 TGCTGTGCTTCCAGAACTAARGGGAAAGCTTTGCCTGAGACCATCGAGGAAGCCGAAATATGCAAGACCA
 AGAAAAAATAAGAAAGATGATTTACCTCCAGTTCAAGAACTAGACATTCCATTGAAC**TAA**GAAGAGAGACC
 GTTGTCTCTCTCATGACAAGGGC

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FIGURE 28

CGGGCCAGGTTTCCAGGCTCGGGCGCCGCTCCATCCCAGCACCTGCGGAGGGAGCCCTGACCAATGGCTCCCTG
 GCCTGAATTGGGAGATGCCCCAGCCCCAACCCGATAAGTAACCTCGAAGGGGGCCGAGGTCAGCAGCCCCACTGCCC
 CTGATAAARAGCAAGAGACCAACAAACAGATAACACTGAGGCACTCTAACCAAGATTGAACCTCTGCCGTCC
 TACTCCACGGCTACACTGATAGATGAGCCCACTGAGGTGGATGACCCCTGGAACCTACCCACTCTPCAGGACTC
 GGGGATCAAGTGGTCAGAGAGAGACACCAAGGGGAAGATTCTCTGTTTCTTCCAGGGATTGGGAGATTGATTT
 TACTTCTCGGATTTCTCTACTTTTCTGTGCTCCCTGGATATTCTTAGTAGGGCTTCCAGCTGTTGGAGGA
 AAAATGSCAGGACAGTTCTTCAGCAACAGCTCTATTATGTCCAACCCCTTTGTTGGGGCTGGTGATCGGGTCT
 GGTGACCGTCTTGGTGCAGAGCTCCAGCACCTCAACGTCCATCGTTGTGACCATGGTGTCTCTCTTCAATTGCTCA
 CTGTTCCGGCTGCCATCCCCATTATCATGGGGGGCAACATTGGAACCTCAATCAOCCACACTATTGTTGCGCTC
 ATGCAGGTGGGAGATCUGAGTGAATTCAGAAGAGCTTTTGCAGGAGCCACTGTCCATGACTTCTTCAACTGGCT
 GTCCGTGTTGGTGTCTTGGCCGTTGGAGGTGGCCACCCATTACCTCGAGATCATAACCCAGCTTATAGTGGAGA
 GCTTCCACTTCAAGAATGGAGAAGATGCCCCAGATCTTCTGAAAGTCATCACTAAGCCCTTCACAAAGCTCAAT
 GTCCAGCTGGATAAAAAAGTTATCAGCCAAATTGCAATGAACGATGAAAAAGCGAARAACAAGAGTCTTGTCAA
 GATTTGGTGCAAAACCTTTTACCAACAAGACCCAGATTAACGTCACTGTTCCTCGACTGCTAACTGCACCTCCC
 CTTCCCTCTGTGAGCGGATGGCATCCAAAACCTGGACCATGAAGAATGTGACCTACAAGGAGAACATCGCCAAA
 TGCCAGCATATCTTTGTGAATTTCCACCTCCCGGATCTTGTGTGGGCAACATCTTCTCATACTCTCCCTGT
 GGTCTCTGTGTTGCTGATCATGATTGTCAAGATCTCTGGGCTCTGTGCTCAAGGGGCGAGTCCGCCACTGTCA
 TCAAGAAGACCATCAACACTGATTTCCCTTTCCCTTGCATGCTTGAAGTGGCTTACCTGGCCATCTCTGTCGGG
 GCAGGCATGACCTTCATCTACAGAGCAGCTCTGTGTTCCAGCTCGGCTTGAACCCCTGATTGGAATCGGCGT
 GATAACCATTTAGAGAGGCTTATCCACTCAGCTGGGCTCCAAACATCGGCAACACACCCGCCATCTGCGCG
 CCTTAGCCAGCCCTGGCAATGCATTGAGGAATTCACTCCAGATCGCCCTGTGCCACTTTTCTTCAACATCTCC
 GGCATCTTCTGTGTTGATCCCGATCCCGTTCACTCGCTGCCCATCCGCATGGGCAAGGGGCTGGGCAACATCTC
 TGCCAAAGTATCGCTGCTTCCCGTCTTCTACCTGATCATCTTCTTCTTCTGATCCCGCTGACCGTGTGTTGGC
 TCTCGCTGGCCGGCTGGCGGTGCTGCTTGGTGTGGGGTTCCTCGTCTTCTCATCATCTCTGTTACTGTGC
 CTCCGACTCCTGCACTCTCGCTGCCACGCGTCTTGGCGAAGAACTCCAGAACTGGAACCTTCTGCGCGCTGTG
 GATGCGCTCGCTGAAGCCCTGGGATGCCGTCTCTCAAGTTCACCGGCTGCTTCCAGATGCGCTGCTGCTACT
 GCTGCCGGGTGTGCTGCCGCGCTGCTGCTTGTGTGGGCTGCCCAAGTGTGCTGCGCTGCAGCAAGTGTGCTGC
 GAGGACTTGGAGGAGGCGCAGGAGGGGCGAGGATGTCCCTGTCAAGGCTCTGAGACCTTTGATACATAACCAT
 TAGCAGAGAGGCTCAGGGTGAAGTCCCTGCCCTCGGACTCAAGAGCCGAATGCACGGCTTGTAGGGGACGCCCC
 AGATTGTCAAGGATGGGGGATGTTCTTGAATTTTGCATGCTCTCTCCCTCCCACTTCTGACCCCTTTCAACC
 ACCTCGAGGAGATTGCTCCCCATTAGCGAATGAAATTCATGCACTCTAAAAA

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FIGURE 29

CAGCCCAGCACCTGCGGAGGGAGCGCTGACCAAGGCTCCCTGGCCCTGAATTGGGAGATGCCAGCCCAACCCCG
 ATAAGTACCTCGAAGGGGCGCGCAGGTGAGCAGGCCACTGCCCTGATAAAAGCAAAGAGACCAACAAAACAGAT
 AACACTGAGGCACCTGTAAACCAAGATTGAACCTTCGCGCTCCACTCCACGGCTACACTGATAGATGAGCCAC
 TGAGGTGGATGACCCCTGGAACCTACCCACTCTTCAGGACTCGGGGATCAAGTGGTCAGAGAGAGACACCAAAG
 GGAAGATTCTCTGTTCTTCCAAGGGATTGGGAGATTGATTTTACTTCTCGGATTCTCTACTTTTTCTGTGTGC
 TCCCTGGATATTCTTAGTAGCGCTTCCAGCTGGTTGGAGGAAAAATGCCAGGACAGTTCTTCAGCAACAGCTC
 TATTATGTCCAACCCCTTTGTTGGGGCTGGTGTATCGGGGTGCTGGTGACCGTCTTGGTGCAGAGCTCCAGCACCT
 CAACGTCCATCGTTGTGTCAGCATGGTGTCTCTTCATGCTCACTGTTCCGGGCTGCCATCCCCATATCATGGGG
 GCCAACATTGGAACGTCAATCACCAACACTATTGTTGCGCTCATGAGGTGGGAGATCGGAGTGASTTCBGAAG
 AGCTTTTSCAGGAGCCACTGTCCATGACTTCTTCAACTGGCTGTCCGTGTTGGTGCCTTGGCCCTGGAGGTGG
 CCAACCCATTACCTCGAGATCATAACCCAGCTTATAGTGGAGAGCTTCCACTTCAAGAATGGAGAAGATGCCCA
 GATCTTCTGAAAGTCATCACTAAGCCCTTCACAAAGCTCATTGTCCAGCTGGATAAAAAAGTTATCAGCCAAAT
 TGCAATGAACGATGAAAAAGCGAAAAACAAGAGTCTTGTCAAGATTGCTGTCBAAACTTTTACCAACAAAGACCC
 AGATTAAAGTCACTGTTCCCTCGACTGCTAACTGCACCTCCCTTCCTCTGTTGGACGGATGGCATCCAAAAC
 TGGACCATGAAGAATGTGACCTFACAGGAGAACATCGCCCAATGCCAGCATATCTTTGTGAATTTCCACCTCCC
 GGATCTTGCTGTGGGACCATCTTGTCTCATACTCTCCCTGCTGGTCTCTGTGCTTGGCTGATCATGATTGTCA
 AGATCCTGGGCTCTGTGCTCAAGGGSCAGGTGCGCACTGTCTCAAGAGACCATCAACACTGATTTCCCTTTT
 CCCTTTGCATGGTTGACTGGCTACCTGGCCATCCTCGTGGGGCAGGCATGACCTTCATCGTACAGASCAGCTC
 TGTGTTCAAGCTCGGCCTTGACCCCTGATTGGAATCGCGGTGATTAACCATTGAGAGGGCTTATCCACTCACCC
 TGGGCTCCAAACATCGGCACCAACACCCGCCATCCTGGCCGCTTAGGCCAGCCCTGGCAATGCATTGAGGAGT
 TCACTCCAGATCGCCCTGTGCCACTTTTCTTCAACATCTCCGGCATCTTGTGTGGTACCCGATCCCGTTCAC
 TCGCCTGCCCATCCGCATGGCCAAGGGGCTGGGCAACATCTCTGCCAAGTATCGCTGGTTCCGCGTCTTCTACC
 TGATCATCTTCTTCTTCCGATCCGCTGACCGTGTGTTGGCCTCTCGCTGGCCGGCTGGCGGGTCTGGTTGGT
 GTCGGGGTTCGGTGGTCTTTCATCATCATCTTCTGCTACTGTGCTCCGACTCCTGCACTCTCGCTGCCACGCGT
 CCTGCCGAAGAACTCCAGAACTGGAACCTTCTGCGCTGTGGATGCGCTCGCTGAAGCCCTGGGATGCGGTG
 TCTCCAAGTTCACCGGCTGCTTCCAGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
 CTGTGTGGCTGCCCCAAGTGTGCTGCGCTGCGCAAGTGTGCTGCGAGGACTTGGAGGAGGGTCAAGAGGGGCAAGGA
 TGTCCCTGTCAAGGCTCCTGAGACCTTTGATTAACATAAACCATTAGCAGAGAGGCTCAGGGGTGAGGTCCCTGCC
 CGGACTCAAAGACCGAATGCACGGCCTTGTAGGGGACGCCCCAGATTGTGAGGGATGGGGGATGGTCTCTGAG
 TTTTGCATGCTCTCCTCCCTCCCACTTCTGCAACCTTCAACCACCTCGAGGAGATTGCTCCCCATTAGCGAAT
 GAAATTGATGCACTCCTACCTAACTCGATTCCCTTTGCTTGGTGGGTAGGCTGCGAGGGCACTTTTATTCCAA
 CCCATGGCTTCCATGACTTTTTCAAAAAABAAAAAABAAAAAABAAAAAABAAAAAABAAAAAABAAAAAAB

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FIGURE 30

[illegible]

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FIGURE 31

CATCTAAAGCCTCCTCAGCCTTCTGAGTCAGCCTGAAAGGAACAGGCCGAACTGCTGTATGGGCTCTACTGCCA
GTGTGACCTCACCCTCTCCAGTCACCCCTCCTCAGTTCAGCTATGAGTTCTGCAACTTCACACATGOCACCT
TTGTGCTTATTGGTATCCAGGATTAGAGAAAGCCCATTTCTGGGTTGGCTTCCCCCTCCTTTCCATGTATGTA
GTGGCAATGTTTGGAAACTGCATCGTGGTCTTCATCGTAAGGACGGAAACGCAGCCTGCACGCTCCGATGTACCT
CTTTCTCTGCATGCTTGCAGCCATTGACCTGGCCCTTATCCACATCCACCATGCCCTAAGATCCTTGCCCTTTTCT
GGTTTGATTCCCGAGAGATTAGCTTTGAGGCCCTGTCTTACCCAGATGTTCTTTATTTCATGCCCTCTCAGCCATT
GAATCCACCATCCTGCTGGCCATGGCCCTTTGACCTTATGTGGCCATCTGCCACCCACTGCGCCATGCTGCAGT
GCTCAACAATACAGTAACAGCCAGATTGGCATCGTGGCTGTGGTCCGGGGATCCCTCTTTTTTTTCCCACTGC
CTCTGCTGATCAAGCGGCTGGCCCTCTGCCACTCCAAATGTCCTCTGCACTCCTATTGTGTCCACCAGGATGTA
ATGAAGTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCAFTCTGCTGCTCATGGGCGT
GGAGCTAATGTTTCATCTCCTTGTCTATTTTTCTGATAATACGAACGGTTCTGCACTGCCCTTCCAAGTCAGAGC
GGGCCAAGGCCCTTTGGAACCTGTGTGTCACACATTTGGTGTGGTACTCGCCCTTCTATGTGCCACTTATTTGCCCTC
TCACTTGTACACCGCTTTGGAAACAGCCCTTCATCCCATTTGTGCTGTTGTCTATGGGTGACATCTACCTGCTGCT
GCTTCTGTCTCATCAATCCCATCTCTATGGTGGCAAAACCAACAGATCAGAACACGGGTGCTGGCTATGTTCA
AGATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGACCCCTTAACACTACACTTCTCCTTATCTTTA
TTGGCTTGATTAACATAATTATTTCTAACACTAGCTTATTTCCAGTTGCCCATAGGCACATCACTACTTTTCTC
TGGCTGGAATAGTAAACTAAAGTATGGTACATCTACCTAAAGGACTATTATGTGGATAATACATACTAATGAA
GTATTACATGATTTAAAGACTACATAAAACCAACATGCTTATAACATTAAAGAAAAACAATAAAGATACATGA
TTGAAACCAASTTGAAAAATAGCATATGCCCTGGAGGAAATGTGCTCAAATTAATAATGATTTAGTGTGTCCC
TACTTTCTCTCTTTTTTCTTTCTTTTTTTTTTATTATGGTTAGCTGTACATACAACTTTTTTTTTTTTTGA
GATGGGCTCTCCAGCCTGGGCAACAGAGCAAGACCTGTCTCAAAGCATAAATGGATTAACATATCAAATGAA
ACAGGGAAATGAAGCTGACAAFTTATGGGAGCCA

[illegible]

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FIGURE 32B

TGATTTCAGACACCCACGAAAACAGTCTTATGGATCAGAATAATCCAATCTCATACTCACTATCTGAGAACTTCTG
 AAGAAGATAATAGAGTTCACAAGTGTATCCTCAGACAGTCAAACTGGTATGGACAGAAAGTCTGGTAAATCACCA
 TCAGCAAAATGGGCTATCCCAAAAGCACAATGATGGAAAAGAGGAAAATGACAFTCAGACTGGTAGTGCTCTGGT
 TCCTCTCAGCCCTGAATCTAAAGCATGGGCAGTTCTGACAAGTGATGAAGAAAGTGGATCAGGGCAAGGTACCT
 CAGATAGCCCTTAATGAGAAATGAGACTTCCACAGATTTCACTTTTGCAGACACTAAATGAAAAGATGCTGATGGG
 ATCCTGGCAGCAGGTGACTCAGAAATAACTCCTGGATTCOCACAGTCCCCAACATCATCTGTTACTAGCGAGAA
 CTCAGAACTGTTCCACGTTTCAGAGGCAGAGGGCCAGTAATAGTAGCCATGAGTCTCGTATTGGTCTAGCTGAGG
 GGTGGAAATCCGAGAGAGAGGCGATTATACCCCTTGGTATGCTGTCAGCCCTGACTTTTATCTGCTAGTGGT
 CTTGTGGGTATTCTCATCTACTGGAGGAAATGCTTCACAGCTGCACACTTTTACTTAGAGGACAGTACATCCCC
 TAGAGTTATATCCACACCTCCAAACACCTATCTTTCCAAFTTCAGATGATGTCGGAGCAATTTCCAATAAAGCACT
 TTCCAAAGCATGTTGCAGATTTACATGCAAGTAGTGGTTTACTGAAGAAATTTGAGACACTGAAAGATTTTAC
 CAGGAAGTGACAGAGCTGACTGTTGACTTAGGTATTACAGCAGACAGCTCCAACCCACCCAGACAAAGCACAA
 GAATCGATACATAAATATCGTTGCCTATGRTCATAGCAGGGTTAAGCTAGCACAGCTTGCTGAAAAGGATGGCA
 AACTGACTGATTATATCAATGCCAATTTATGTTGATGGCTACACAGACCCAAAGCTTATATTTGCTGCCCAAGGC
 CCACTGAAATCCACAGCTGAAGATTTCTGGAGAATGAATGGGAACATAATGTGGAAGTTATTTGTCATGATAAC
 AAACCTCGTGGAGAAAGGAAGGAGAAATGTGATCAGTACTGGCCTGCCGATGGGAGTGAGGAGTACGGGAAT
 TTCTGGTCTCTCAGAGAGTGTGCAAGTGTCTTGCCTATTATCTGTTGAGGAATTTTACTCTAAGAAACACAAAA
 ATAAAAAAGGGCTCCCAAGAAAGGAAGACCCAGTGGACGTGTGGTCAACACAGTATCACTACACCCASTGGCCTGA
 CATGGGAGTACCAGAGTACTCCCTGCCAGTGTCACTTTTGTGAGAAAGGCAGCCTATGCCAAGCGCCATGCAG
 TGGGGCCTGTTGTCTCCTACTGCAGTGTGGAGTTGGAGAACAGGCACATATATTTGTGCTAGACAGTATGTTG
 CAGCAGATTCAACACGAAGCACTGTCAACATATTTGGCTTCTTAAAAACACATCCGTTCCACAAAGAAATATTT
 GGTACAAACTSAGGAGCAATATGTCTTCATTTCATGATACACTGCTTGGAGGCCATACTTAGTAAAGAACTGAGG
 TGCTGGACAGTCAATATTCATGCCATATGTTAATGCACTCCTCATTCCTGGACCAGCAGGCCAACAAGCTAGAG
 AAACAATTCAGCTCCTGAGCCAGTCAATATATACAGCAGAGTCACTATTTCTGAGCCCTTAAAGCAATGCAACAG
 GGAAAAAGAAATCGAATCTCTCTATCATCCCTGTGGAAAGATCAAGGGTTGGCATTTTCATCCCTGAGTGGAGAG
 GCACAGACTACATCAATGCCCTCTATATCATGGGCTATTTACAGAGCAATGAATTCATCATTACCCAGCACCT
 CTCTCTCATACCATCAAGGATTTCTGGAGGATGATATGGGACATAATGCCCAACTGGTGGTTATGATTCCTGA
 TGGCCAAAACATGGCAGAGATGAATTTGTTTACTGGCCAAATAAAGATGAGCCTATAAATGTGASAGCTTTA
 AGGTCACTCTTATGGCTGAGAAACACAAATGTCTATCTAATGAGGAAAACTTATAATTCAAGACTTTATCTTA
 GAAGCTACACAGGATGATTATGTAATGAAGTGAGGCACTTTCAGTGTCTTAAATGGCCAAATCCAGATAGCCC
 CATTAATAAACTTTTGAATTTATAAGTGTATAAAGAAAGAGCTGCCAATAGGGATGGGCTATGATTTGTTT
 ATGATGAGCATGGAGGATGACGGCCAGGAATTTCTGTGCTCTGACAACCTTATGCACCACTAGAAAAAGAA
 AATTCCTGGATGTTTACCGCTAGCCAGATGATCAATCTGATGAGGCCAGGAGTCTTTGCTGACATTAAGCA
 GTATCACTTTCTCTACAAAGTGATTCCTCAGCCTTGTGAGSCACAGGCAGGAAGAGAAATCCATCCACCTCTCTGG
 ACAGTAATGGTGCAGCATTGCTGATGGAAATATAGCTGAGAGCTTAGAGTCTTTAGTTTAAACACAGAAAGGGG
 TGGGGGGAATCACATCTGAGCATGTTTCTCTCTTCTTAAATAGGCAGGAAATCAGTCTAGTTCTGTTTATC
 TGTGATTTCCCATCACCTGACAGTAATTTTCATGACATAGGATTTCTGCCGCCAATTTATATCAITTAACAATG
 TGTGCTTTTTCAGAGACTTGTAAATTTACTTATTATGTTTGAATTAATATGATTTTACAGTATTTCTAA
 CAATGGAAATGTGCTATTTTCTCTATTTGATTTTACAGAAATTTCAATTTATAGAGGTTAGGAATCCAA
 ACTACAGAAATGTTTGTCTTTTASTGTCAAATTTTATGCTGATTTTGTAGCAATTTATCAGTTTGTCTAGAAATA
 TAATTTTATACAGTAGCCTGTAAATTAACAACTCTTCCATATGATATTCACATTTTACAACTGCAGTATTC
 ACCTAAAGTAGAATAATCTGTTACTTATTGTAATACTGCCCCAGTGTCTCCATGGACCAATTTATATTTAT
 AATTGTAGATTTTATATTTTACTACTGASTCAAGTTTTCTAGTTCTGTGTAATTTGTTTATTTAATGAGGTAG
 TTCATTAGCTGGTCTTACTCTACCAGTTTTCTGACATTTGATTTGTTTACCTAAGTCAATTAATTTGTTTCAGC
 ATGTAATTTTAACTTTTGTGGAAATAGAAATACCTTCATTTTGAAGAGTTTTTATGAGAAATACACCTTAC
 CAAACATTTGTTCAAATGTTTTTATCCAAGGAATTCAAAATAAATATATATATTTCCATTAABAAAAA
 AAAAAA

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FIGURE 33

[illegible]

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FIGURE 34

ACGCGTCCGCCCCACGCGTCCGCCCCACGCGTCCGCGTCCGGGCCCCAGAGCCGAGGTGTACCTGGCGGCCCGTGGTGGG
 GCACCTGACCGCCGAGATCCCTGGAGCTGGCTGGCAACCCGGCCCCGACACAAGAAGACCCGCGATCATCTCTGGCCC
 ACCTGTAGCTGGCCATTTCGCAACGGCGAGGAGCTTAACAAGCTGCTGGGCGAAGTCACCATCGCGCAGGGCGGT
 GTCCCTGCCCAACATTTCAGGGCGTGTCTCTGCCCCAGAGACCAAGAGCCACCCACAAGGCCAAGGGTGAAAACCA
 TTCCTAGGAGAGAGAGAAACACAATGGGCCACCAAGACAGAGTTGAGTCCCACAGCAAGGGAGAGCAGAGAACCA
 CAAGATATGCAAGTGGATGAGACACTGATCCCCAGGAAAGGTCCAAGTTTATGTTCTGCTCGCTATGGATAGC
 CCTCGTCTTACATTTCTGCAATTTCAACAGATAGCACAAATGTCTCATGAAATCACCATGGTAGCCATGG
 TCAACAGCACAAAGCCCTCAATCCCAGCTCAATGATTCTCTGAGGTGCTGCCCTGTTGACTCATTTGGTGGCCCTA
 AGTAAAGCCCCAAGAGTCTTCTCTCAAAAGTCCCTCAATACTGGGGGTCAAGTTTCAATTTGGGAAAAGTGGGG
 CCGCTCCACAAGAACGAGCAGACTCTGCAGCATTTGCTTTATCAGGAATGTTACTGGGATGCTTTACTGCCATCC
 TCATAGGTGGCTTCATTAAGTGAACCCCTTGGGTGGCCCTTTGTCTTCTATATCTTTGGAGGTGTTGGCTGTGTC
 TGCTGCCCTTCTCTGCTTTGTTGATTTATGATGACCCCTTTTCTCTATCCATGGATAAGCACCTCAGAAAAGA
 ATACATCATATCTCTCTTGAACAACAGGTCCGGTCTTCTAAGCAGCCCTCTTCCCATCAAAAGCTATGCTCAGAT
 CTCTACCCATTTGGTCCATATGTTTAGGCTGTTTCAGCCATCAATGCTTAGTTAGCCAAATGCTTGTATACATA
 CCAACTTACATCAGCTCTGTGTACCATGTTAACATCAGAGACAATGGACTTCTATCTGCCCTTCCTTTTATTGT
 TGCCTGGGTCAAGGATGGTGGGAGGCTATCTGGCAGATTTCTCTTAACCAAAAAGTTTAGACTCATCACTG
 TGAGGAAATTTGCCACATTTTAGGAAGTCTCCCTCTTCAGCACTCATTGTCTCTCTGCCCTTACCTCAATTCG
 GGCTATATCACAGCAACTGCCCTTGTCTGACGCTCTCTTGGGGATTAAAGCACATTGTGTCAAGTCAAGGATTATAT
 CAATGTCTTAGATATGCTCCCAAGGTATTCCAGTTTTCTCATGGCAGCATCAAGAGGATTTTCAGCATAGCAC
 CTGTCAATTGTACCCACTGTGAGCGGATTTCTTCTTAGTCAGGACCCCTGAGTTTGGGTGGAGGAATGCTTCTTC
 TTGCTGTTTGGCGTTAAOCTGTTAGGACTACTCTTCTACCTCATATTTGGASAAAGCAGATGTCCAGAAATGGCC
 TAAAGAGAGAAAACCTCACTCGTTTATGAGAGTTATCCCACCTTGGATGGAAAAGTCATTAGGCACCGTATTGCAT
 AAAATAGAAGGCTTCCGTGATGAAAATACAGTGAAAAGATTTTTTTTTCTCTGTGGCTCTTTTCAATTATGAGA
 TCAGTTCATTATTTTATTCAGACTTTTTTTTGGAGAGAAATGTAAGATGAATAAAAATTCAAATAAATGATAAC
 TAAGAAAAAABAAAAA

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FIGURE 35

GTGAAAACCATTTCACTAGGAGAGGGGAAAACACABTGGGCCACCAAGACAGAGTTGAGTCCCACAGCAAGGGAGAG
CAAGAACGCACAAGATATGCAAGTGGATGAGACACTGATCCCCAGGAAAGTTCCAAGTTTATGTTCTGCTCGCT
ATGGAATAGCCCTCGTCTTACATTTCTGCAATTTACAAACGATAGCACAAAATGTCATCATGAACATCACCATG
GTAGCCATGGTCAACAGCACAAAGCCCTCAATCCCAGCTCAATGATTCTCTGAGGTGCTGCCCTGTTGACTCATTT
TGGTGGCCTAAGTAAAGCCCCAAAGAGTCTTCTACAAAGTCTCAATFACTTGGGGGTCAAGTTTGCAATTTGGG
AAAAGTGGGGCCCTCCACAAGAACGAAGCAGACTCTGCAGCATTGCTTTATCAGGAATGTTACTGGGATGCTTT
ACTGCCATCTCTCATAGGTGGCTTCATTAGTGAACCCCTTGGGTGGGCCCTTTGTCTTCTATATCTTTGGAGGTGT
TGGCTGTCTGTCTGCTGCCCTCTCTGCTTGTGTTGATTTATGATGACCCCTTTCTCTATCCATGGATAAGCACCT
CAGAAAAAGAAATACATCATATCTCTCTTGAACACAGGTGAGGTCTTCTAAGCAGCCCTCTTCCCATCAAGCT
ATGCTCAGATCTCTACCCATTTGGTCCATATGTTTAGGCTGTTTCAGCCATCAATGGTTAGTTAGCACAAATGGT
TGTATACATACCAACTTACATCAGCTCTGTGTACCATGTTAACATCAGAGACAAATGGACTTCTATCTGCCCCCTC
CTTTTATGTTGCCCTGGCTCATAGGCATGGTGGGAGGCTATCTGGCAGATTTCCTTCTAACCAGAAAGTTTAGA
CTCATCACTGPGAGGAAAATTGCCACAATTTTAGGAAGTCTCCCTCTTCAGCACTCATTTGTGTCTCTGCCCTTA
CCTCAATTCGGCTATATCAGCAACTGCCCTGCTGACGCTCTCTTGGGGATTAGCACATTGTGTCAAGTCAG
GGATTTATATCAATGTCTTAGATATTGCTCCAAGGTATTCAGTCTTCTCATGGGAGCATCAAGAGGATTTTCG
AGCATAGCACCTGTCAATGTACCCACTGTGACGGGATTTCTTCTTAGTCAGGACCCCTGAGTTTGGGTGGAGGAA
TGTCTTCTCTTCTGCTGTTTGGCCCTTAACCTGTTAGGACTACTCTTCTACCTCATATTTGGAGAAGCAGATGTCC
AAGAATGGGCTAAAGAGAGAAAAGTCACTCGTTTATGAGTATCCCACCTTGGATGGAAAAGTCATTAGGCAC
CGTATTGCATAAAATAGAAGGCTTCCGTGATGAAAATACCACTGAAAAGATTTTTTTTTCTGTGGCTCTTTTC
AATTATGAGATCAGTTCAATATTTTATTGAGCTTTTTTTTGAAGAAATGTAAGATGAATAAAATTCAAATA
AAATGATACTAAGAAAAA

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FIGURE 36

[illegible]

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FIGURE 37

ATTGCGCCCTTTGCTCCCGGGTGTCCAGGGCCCGCCGGTGGCAGAGCAATGGCGGGTGCGGGCCCGAAGCGGGG
 CGCGCTAGCGGCGCCGGCGGGCCGAGGAGAAAGGAGAGGGCGCGGGAGAAGATGCTGGCGGCCAAGAGCCCGGACG
 GCTCGGCGCGCGCGAGGGCGAGGGCGGTGACCCCTGCAGCGGAACATCACGCTGCTCAACGGCGTGGCCATC
 ATCGTGGGGACCAATATCGGGCTCGGGCATCTTCGTGACGCCCACGGGCGTCTCAAGGAGGCAGGCTCGCCGGG
 GCTGGCGCTGGTGGTGTGGGCGGCGGTGCGGGCTCTTCTCCATCGTGGGCGCGCTCTGCTACGGCGAGCTGGCA
 CCACCATCTCCAAATCGGGCGGGGACTACGGCTACATGCTGGAGGTCACGGCTCGCTGCCCCGCTTCTCTCAAG
 CTCTGGATCGAGCTGCTCATCATCCGGCCTTCATCCAGTACATCGTGGCCCTGGTCTTGGCCACCTACCTGCT
 CAAGCCGCTCTTCCCCACCTGCCCCGGTGGCCGAGGAGGCGAGCCAAAGCTCGTGGCCTGCCTCTGCGTGTGCTGC
 TCACGGCCGTGAAGCTGCTACAGCGTGAAGGCGCGCCACCCGGCTCCAGGATGCTTTGCGCGCGCCAGCTCCTG
 GCCCTGGCCCTGAFCATCCTGCTGGGCTTCGTCCAGATCGGGGAGGGTGTATGTGTCCAATCTAGATCCCAACTT
 CTCATTTGAAGGCGCCAAACTGGATGTGGGGAACATTGTGCTGGCATTATACAGCGGCTCTTTGCTATGGAG
 GATGGAATTACTTGAATTTGCTCACAGAGGAATGATCAACCCCTACAGAAACCTGCCCCCTGGCCATCATCATC
 TCCCTGCCCATCGTGACGCTGGTGTACGTGCTGACCAACCTGGCCTACTTCACCAACCTGTCCACCGAGCAGAT
 GCTGTGCTCCGAGGCGGTGGCCCTGGACTTCGGGAACATATCACCTGGGCGTCATGTCTGGATCATCCCCGTCT
 TCGTGGGCTGTCTGCTTGGGCTCCGTCAATGGGTCCCTGTTACATCCTCCAGGCTCTTCTTCTGTTGGGTCC
 CGGGAAGGCCACCTGCCCTCCATCCTCTCCATGATCCACCCACAGCTCCTCACCCTCGTGGCGTCCCTCGTGT
 CAGCTGTGTGATGACGCTGCTCTACGCCCTTCTCCAGGACATCTTCTCCGTCTCAACTTCTTCAGCTTCTTCA
 ACTGGCTCTGCGTGGCCCTGGCCATCATCGGCATGATCTGGCTGGCCACAGAAAGCCTGAGCTTGAGCGGCCC
 ATCAAGGTGAACCTGGCCCTGCTGTGTTCTTCATCCTGGCTGCTCTTCTGATCGCCGTCTCTCTGGA
 GACACCCGTGGAGTGTGGCATCGGCTTCACCATCATCTCAGCGGCTGCCCGTCTACTTCTTCGGGCTCTGGT
 GGAAAAACAAGCCCAAGTGGCTCCTCCAGGGCATCTTCTCCAGGACCTCTGTGTGAGAAGCTCATGCAGGTG
 GTCCCCCAGGAGACATAGCCAGGAGGCCGAAGGCG

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FIGURE 38

CCAGGCTCTCCACCCCCACTTCCCATTGAGGAAACCGAGGCAGAGGAGGCTCAGGTGTGGCCATCACCCCTGC
 ACATCAGAGTTACCCCTGGGCAGGGCCCCACTGAGACCTGGGAGGGGGCCACTCGGGACCTGGAGGGCTGGGGGCTG
 CCGGGGCTTAGGGGFAAAGCTCCCTACCCCACTGCGCAGAAAGGCCTCAGAGGCCTGGGGGCTGGGCTTCCCTT
 TTCACATCGCCCTTACAGAGGCCCACTGTGGGCATTGGCCCCGATCTGAAAGGGGCTGTCTGTTCCTCATGG
 GCGCTGCCAGGCCACGCACTCCTCTTCTGCTGGCCGGCCCACTCCCTCTGCTGTGAGCGCGGACAGAGAG
 CTACCGGTGGACCCACGGTGCCTCCCTCCCTGGGATCTACACAGACCAAGGCTTGGCCAAAGGCTCGACCCCTG
 TTGGGGTCTCTGGGACCCCCCGCCCTCGGCAGCCCTCCCTGTTCTCTGCTCTTCAGCCCTCGGATGGGTGCAGCCCTC
 GAGGACCTTGGCTGGAGAGACAGGGCAGGAGGCTGCACCCCTGGACGGAGTCTTGGCCAAACCCACCTAACATTT
 CCAGCCTCTCCCTCAGCAACTCCTTGGCTTCCCTGTGCGGAGGTGTCCGGCTGAGCAGGAGGCTGTCCGG
 GAGCTGGCTGTGGCTTGGCAGAGAAATGTCAAGCTCTCAACAGAGCAGCTGGGCTGTCTGGCTCACCGGCT
 CTCTGAGCCCCCGAGGACCTGGACGCCCTCCCATTTGAGCTGCTGCTATTCTCAACCCAGATGGCTTCTCGG
 GGGCCAGGCTGACCCGTTTCTTCTCCCGCATCAGGAGGCCAATGTGGACCTGCTCCCGAGGGGGGCTCCG
 GAGGACAGCGGCTGTGCTGCGCTCTGGCTGCTGGGGTGTGCGGGGCTCTCTGCTGAGCGAGGCTGATGT
 GCGGGCTCTGGGAGGCTGGCTTGGACCTGCTGGGCGCTTGTGGCCGAGTGGGCGGAGTGTGCTACCCC
 GCTGTGTGAGCTGCCCCGGGACCCCTGGACACAGGACAGCAGGAGCCAGCCAGGGCGGCTCTGCGGGGGGGGA
 CCCCCCTACGGCCCCCGCTCGACATGGTCTGTCTCCAGATGGAAGCTCTGCGGGGCTGTGCCCCGTGTGGG
 CCAGCCCATCATCCGAGCATCCCCGAGGGCATCGTGGGCGCTGGCGGCAAGCTCTCTCGGGACCCATCCT
 GCGGCGACCTGAACGGACCTTCTCCGGCGCGGTTCCGGCGGGAAGTGGAGAAGACAGGCTGTCTTCAAGC
 AAGAGGCCCCCGAGATAGACAGAGCCCTCATCTTCTACAAGAAGTGGAGCTGGAAGCCTGCTGGATGCGGC
 CCTGTGCTCCACCCAGATGGACCGGTGAACGCCATCCCTTACCTACGAGCAGCTGGACGTCTTAAGCATA
 AACTGGATGAGCTCTACCCACAAGGTTACCCGAGTCTGTGATCCAGCAGCTGGGCTACCTCTTCTCAAGATG
 AGCCCTGAGGACATTGCAAGTGGATGTGACCTCCCTGGAGACCTGAAGGCTTGTCTTGAAGTCAACAGAGG
 GCACGAAATGAGTCTCAGGTGGCCACCCGTGATCGACCGCTTGTGAGGGGAAGGGGCCAGCTAGACAGAGCA
 CCTAGACACCCCTGACCGCTTCTACCCCTGGGTACCTGTGCTCCCTCAGCCCCGAGGAGCTGAGCTCCGTGCCC
 CCCAGCAGCATCTGGGGGCTCAGGCCCCAGGACCTGGACACGTGTGACCCAGGCGAGCTGGACGTCTCTATCC
 CAAGGCCCCGCTTGTCTTCCAGACATGAACGGGTCCGAATACTTCTGAGAGATCCAGTCTTCTCTGGGTGGGG
 CCCCCACGGAGGATTTGAAGGCGCTCAGTCAGCAGAAATGTGAGCATGGACTTGGCCAGCTTCTATGAGCTGCGG
 ACGGATGCGGTGCTCCGTTGACTGTGGCTGAGGTGCAGAACTTCTGGGACCCCTCGTGGAGGGCTGAGGGC
 GGAGGAGCGGCACCGCCCGGTGCGGACTGGATCCTACGGCAGCGGAGGAGACCTGGACACGCTGGGGCTGG
 GGCTACAGGGCGGCTACCCCAACGGCTACCTGGTCTAGACCTCAGCTGCAAGAGGGCCCTCTCGGGGACGCCC
 TGCTCTAGGACCTGGAACCTGTTCTCACCGTCTGSCACTGCTCTAGCTCCACCTTGGCTGAGGGCCCCA
 CTCCCTTGTGGCCCCAGCCCTGCTGGGGATCCCGCTGGCCAGGAGCAGGCACGGGTGATCCCGTCTCCAC
 CCAAGAGAACTCGCGCTCAGTAAACGGGAACATGCCCCCTGCAGACAGCTAAAAAABAAAAA

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FIGURE 39

TGGGATCTACACAGACCATGCGCCTTGCCAAAGGCTCGACCCCTGTTGGGGTCTCTGTGGGACCCCGCCCTCGGCAGC
 CTCTCTGTTCTCTGCTCTTCAGCCTCGGATGGGTGCAGCCCTCGAGGACCTCTGGCTGGAGAGACAGGGCAGGAGGC
 TGGCCCCCTGGACGGAGTCTCTGGCCAAACCCACCTAACATTTCCAGCCTCTCCCTCGCCAACTCTTGGCTTCC
 CGTGTGCGGAGTGTCTCGGCCTGAGCACGGAGCGTGTCCGGGAGCTGGCTGTGGCCTTGGCACAGAAGATGTC
 AAGCTCTCAGACAGAGCAGCTGCGCTGTCTGGCTCACCGGCTCTCTGAGCCCCCGAGGACCTGGACGCCCTGCC
 ATTGGACCTGCTGCTATTCTCAACCCAGATGCGTTCCTCGGGGCCCCAGGCCCTGCACCCGTTTCTTCTCCCGCA
 TCACGAAGGCCAATGTGGACCTGCTCCCAAGGGGGGCTCCCCGAGCGACAGCGGCTGCTGCTGCGGCTCTGGCC
 TGCTGGGGTGTGCGGGGGTCTCTGCTGAGCGAGGCTGATGTCCGGGCTCTGGGAGGCCCTGGCTTGGACCTGCC
 TGGGCGCTTTGTGGCCAGTCCGCCGAAGTCTGCTACCCCGGCTGGTGAGCTGCCCGGACCCCTGGACCCAGG
 ACCAGCAGGAGGACCCAGGGCGGCTCTGCGAGGCGGGGGACCCCCCTACGGCCCCCTCGACATGGTCTGTCTC
 TCCACGATGGACGCTCTCGGGGCTGCTGCCCGTGTCTGGGCCAGCCCATCATCCGACGATCCCGCAGGGCAT
 CGTGGCCGCTGGCGGCAACGCTCTCTCGGGACCCATCTTGGCGGCAGCCTGAACGGACCATCTCTCGGGCGC
 GGTTCGCGCGGGAAGTGGAGAAGACAGCCTGTCTTCAGGCCAAGAGGCCCGGAGATAGACGAGAGCCTCATC
 TTCTACAAGAAGTGGGAGCTGGGAGCCTGCGTGGATGCGGCCCTGCTGGCCACCGAGATGGACCGCGTGAACGC
 CATCCCCCTTACCTACGAGCAGCTGGACGTCCTAAAGCATAAACTGGATGAGCTCTACCCACAGGTTACCCCG
 AGTCTGTGATCCAGCAGCTGGGCTACCTCTTCTCAAGTGAAGCCTGAGGACATTCCGAAGTGGAAATGTGACG
 TCCCTGGAGACCCCTGAAGGCTTTGCTTGAAGTCAACAAAGGSCACGAAATGAGTCTCAGGTTGGCCACCCCTGAT
 CGACCGCTTTGTGAAGGGAAGGGGCTAGCTAGACAAAGACACCCCTAGACACCCCTGACCGCCTTCTACCCCTGGGT
 AACTGTGCTCCCTCAGCCCCGAGGAGCTGAGCTCCGTGCCCCCAGCAGCATCTGGGCGGTGAGGCCCCAGGAC
 CTGGACACGTTGTGACCCAAGGCGAGCTGGACGTCCTCTATCCCAAGGCCCCGCTTGTCTTCCAGAACATGAACGG
 GTCCGAACTACTTCGTGAAGATCCAGTCCCTTCTGGGTGGGGCCCCCAGGAGGATTTGAAGGCGCTCAGTCAGC
 AGAATGTGAGCATGGACTTGGCCACGTTGATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAG
 GTGCAGAACTTCTGGGACCCACGTCGAGGGGCTGAAGGCGGAGGAGCGGCACCGCCCCGTGCGGACTGGAT
 CCTACGBCAGCGGCAGGACGACCTGGACACGCTGGGGCTGGGCTACAGGGCGGCATCCCCAAGGCTACCTGG
 TCTAGACCTCAGCGTGCAAGAGGCCCTCTCGGGGACGCCCTGCTCTAGGACCTGGACCTGTTCTACCGTC
 CTGGCACTGCTCTAGCCTCCACCCCTGGCTGAGGGGCCCCACTCCCTTGTGCGCCCCAGCCCTGCTGGGATCC
 CCGCCTGGCCAGGAGCAGGACAGGCTGATCCCTCTCCACCCCAAGAGAACT

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FIGURE 40

ATATCAGCATGAAGTGGCGTGGAACTGGAAATAGGGCTGTCTCTCCCTCGACCTCCCOCTCCTTGTCCCTCTG
 CTCACCCCTCGCTCGTTCCCTCCCTCCGGCGAGGGCGCCCTTTATAACAACCTGCTCAGAGTSCGAGGGCGGGAT
 AGCTGTCCAAGGTCTCCCCCAGCACTGAGGAGCTCGCCTGCTGCCCCTCTTGCGCGCGGGAGCAGCACCAAGTT
 CACGGCCCAACGCCTTGGCACTAGGGTCCAGAAATGGCTACAAACAGTCCCTGATGGTTGCCGCAATGGCCTGAAT
 CCAAGTACTACAGACTTTGTGATAAGGCTGAAGCTTGGSSCATCGTCCAGAAACGGTGGCCACAGCCGGGGTT
 GTGACCTCGGTGGCCTTCATGCTCACTCTCCCGATCCTCGTCTGCAAGGTSCAGGACTCCAACAGSCGAAAAAT
 GCTGCTACTCAGTTTCTCTTCCCTCGGTGTGTTGGGCATCTTGGGCTCACCTTCGCCCTCATCATCGGAC
 TGGACGGGAGCACAGGGCCACACGCTTCTTCTCTTTGGGATCCTCTTTCCATCTGCTTCTCCTGCTGCTG
 GCTCATGCTGTGAGTCTGACCAAGCTCGTCCGGGGAGGAAGCCCCCTTCCCTGTTGGTGAATCTGGGCTCTGGC
 CGTGGGCTTCAGGCTAGTCCAGGATGTATCGCTATTGAATATATTGTCTGACCATGAATAGSACCACGCTCA
 ATGTCTTTCTGAGCTTTCCGCTCCTCGTCCCAATGAAGACTTTGTCTCTCTGCTCACCTACGCTCTTCTTG
 ATGGCGCTGACCTTCCCTCATGTCTCTCTCACCTTCTGTGTTCTCTTCACGGCTGGAAGAGCATGGGGCCCA
 CATCTACCTCACGATGCTCCTCTCCATGGCATCTGGGTGGCCTGGATCAGCCTGCTCATGCTTCTCTGACTTTG
 ACCGCAGGTGGGATGACACCATCCTCAGCTCCGCTTGGCTGCCAATGGCTGGGTGTTCTGTTGGCTTATGT
 AGTCCCGAGTTTGGCTGCTCACAAAGCAACGAAACCCCATGGATTATCCTGTTGAGGATGCTTTCTGTAAAC
 TCAACTCGTGAAGAGAGCTATGGTGTGGAGACAGAGCCTACTCTCAAGAGGAATCACTCAAGGTTTTGAAG
 AGACAGGGGACACGCTCTATGCCCCCTATTCCACACATTTTCAGCTGCAGAACCCAGCTCCCCAAAAGGAATTC
 TCCATCCACAGGGCCACGCTTGGCCGAGCCCTTACAAAGACTATGAAGTAAAGAAAGAGGGCAGCTAACTCTG
 TCCTGAAGAGTGGGACAAATGCACCCGGGGCGCCAGATCTAGCGGAGCTCRAAGGGATGTGGGGCAATCTTGA
 GTCTTCTGAGAAAACGTGTACAAGACACTACGGGACAGTTTGCCTCCCTCCAGCCTCAACCACAATCTTCCA
 TGCTGGGGCTGATGTGGGCTAGTAAGACTCCAGTTCTTAGAGGCGCTGTAGTATTTTTTTTTTTTGTCTCATC
 CTTTGGATACTTCTTTAAGTGGGAGTCTCAGGCAACTCAAGTTTAGACCCCTACTCTTTTGTGTTTTTTG
 AAACAGGATCTTGTCTGTGTCACCCAGGCTTGAAGTGCAGTGGTGGATCACAGCCAGTGCAGCCTCGACCACT
 GTGCTCAAGCAATCCTCCCATCTCCATCTCCCAAGTGCCTGGGATGACAGGCGTGAGCCACAGCTCCAGCCTA
 GGCCCTTAATCTTGTCTGTTATTTCCATGGACTAAAGGTCTGGTCACTGTAGCTCAGGCTGGCTCACACAGCTC
 TAGGGGCTGCTCCTCTAACTCACAGTGGGTTTTGTGAGGCTCTGTGGCCAGAGCAGACCTGCATATCTGAGC
 AAAAATAGCAAAAGCCTCTCTCAGCCCACTGCGCTGAATCTACACTGGAAAGCCAACTTGTGGGACCCCCGCTC
 CCCAACCCTTCTTGCCTGGGTAGGAGAGGCTAAAGATCACCCCTAATTTACTCATCTCTCTAGTGTGCTCTCAC
 APTGGGCTCAGCAGCTCCCCAGCACCATTACAGGTCAACCCCTCTCTTCTTGCAGTGTCCCCAAACTTGTG
 TCAATTCGAGATCTAATCTCCCCCTACGCTCTGCCAGGAATCTTTCAAGACCTCACTAGCACAAGCCCCGTTG
 CTCCTTGTGAGGAGAAATTTGTAGATCAATCTCACTTCAAATTCCTGGSSCTGATACTTCTCTCATCTTGCACCC
 CAACCTCTGTAAATAGATTTACGCAATTTACGGCTGCATTTCTGTAAAGTGGGATGCTCTCCTAATGGAGGAGTG
 TTCAATGTATAATAAGTTATTCACCTGAGTATGCAATAAGATGTGGTGGCCACTCTTTCATGGTGGTGGCAGC
 AAAAAAAAAAAAAA

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FIGURE 41

AGAGACTCAAGATGATTCCCTTTTACCCATGTTTTCTCTACTATTGCTGCTTATTGTTAACCCTATACAGCC
 AACAAATCATTATGACAAGATCTTGGCTCATAGTCGTATCAGGGGTCGGGACCAAGGCCAAATGTCGTGCCCC
 TCAACAGATTTTGGGCACCAAAAAGAAATACTTCAGCACTTGTAAAGAACTGGTATAAAAAGTCCATCTGTGGAC
 AGAAACGACTGTTTTATATGAATGTTGCCCTGGTTATATGAGAAATGCAAGGAATGAAAGGCTGCCAGCAGTT
 TTGCCCCATTGACCATGTTTATGSCACTCTGGGCATCCTGGGAGCCACCACAACGACGCTATTCTGAAGCCTC
 AAACTGAGGGAGGAGATCGAGGGAAAGGGATCCTTCACTTACTTTGCAACGAGTAATGAGGCTTGGGACAACT
 TGGATTCTGATATCCGTAGAGGTTTGGAGAGCAACGTAATGTTGAATTACTGAATGCTTTACATAGTCACATG
 ATTAATAAGAGAATGTTGACCAAGGACTTAAAAAATGGCATGATTATTCTTCAATGTATAACAATTTGGGGCT
 TTTCAATTAACCATTAATCTTARTGGGGTTGTCACTGTTAATTGTGCTCGAATCATCCATGGGAACAGATTGCAA
 CAAATGGTGTTCATGTCATTGACCGTGTGCTTACACAAATTTGGTACCTCAATTCAAGACTTCATTGAAGCA
 GAAGATGACCTTTTATCTTTTAGASCAGCTGCCATCACATCGGACATATTGGAGGCCCTTGGAGAGACGGTCA
 CTTCCACACTCTTTGCTCCCAACCAATGAGGCTTTTGAGAAACTTCCACGAGGTGTCTTAGAAGGTTCAATGGGAG
 ACAAGTGGCTTCCGAAGCTCTTATGAGTACCACATCTTAAATACTCTCCAGTGTCTGAGTCTATTATGGGA
 GGAGCAGTCTTTGAGAGCTTGGAGGCAAAATACAATTTGAGTACCATGTGACGCTGACAGTATAACAGTAATGG
 AATCAAAATGCTGAACAAAAGGATATTGTGACAAATTAATGGTGGATCCATTTGATTGATCAGGTCCTAATTC
 CTGATTCCTGCCAAACAAGTTATTGAGCTGGCTGGGAAACAGCRAACACCTTCAAGGATCTTGTGGCCCAATTA
 GGCTTGGCATCTGCTCTGAGGCCAGATGGAGAAATACACTTTGCTGGCACCCTGTGAATAATGCATTTTCTGATGA
 TACTCTCAGCATGGTTGAGCGCCTCCTTAAATTAATTCTGCAGAAATCACATATTGAAAGTAAAGTTGGCCTTA
 ATGAGCTTTTCAACGGGGCAAAATACTGGAAACCTCGGAGGCAAAACAGCTCAGAGTCTTCTGTATATCTGACAGCT
 GTCTGCATTGAABATTCATGCTGGGAAAGGAGTAAGCAAGGGAGAAACGGTGGCATTCACTATTTCGGCGA
 GATCATCAABCCAGCAGAGAAATCCCTCCATGAAAAGTTAAACAAGATAAGCGCTTTAGCACCTTCTCAGCC
 TACTTGAAGCTGCAGACTTGAAGAGGCTCCTGACACACCTGGAGACTGGACATTTATTGTGCCACCAATGAT
 GCTTTTAAAGGGAATGACTAGTGAAGAAAAAGAAATCTGTATACGGGACAAAATGCTCTTCAAAACATCAATCT
 TTATCACCTGACACCAGGAGTTTCAATTGGAAGGAAATTTGAACCTGGTGTACTAACATTTTAAAGACCACAC
 AAGGAGCAAAATCTTCTGAAAGAAAGTAATGTATCACTTCTGGTGAATGAATTGAATCAAAAGAATCTGAC
 ATCAHACACAAATGCTGTAATTCATGTTGTAGTAAACTCCTCTATCCAGCAGACACCTGTTGGAATGA
 TCACTGCTGGAATACTTAAATTAATCAAATACATCCAAATTAAGTTTGTTCGTTGGTAGCACCTTCAAAG
 AAATCCCCGTGACTGTCTATACAACTAAATTTATAACCAAAGTTCTGGAACCAAAATTAAGTERTTGAAGGC
 AGTCTTCAGCCTATTATCAAAACTGAAGGACCCACACTAACAAAGTCAAAATTTGAAGGTTGAACCTGAATTCAG
 ACTGATTAAGAAGGTTGAACAAATACTGAAGTGTATCCATGGAGAGCCAAATTTTAAAAAATACACCAAAATCA
 TTGATGAGTSCCTTGGGAAATTAATGAAAAAGAGACACGAGAGAAACGAATCATTACAGGTCCTGAATAAAA
 TACACTAGGATTTCTACTGGAGCTGGACARACAGAGAAACTCTGAAGAAATTTGTACAGAGAGAGGTCAACAA
 GGTCAACAAATTCATTGAAGGTTGGTATGCTCATTTATTGAAGATGAAGAAATTTAAAGACTGCTTCAGGGAG
 ACACACCCGTGAGCAAGTTGCCAGCCACAAAAAGTTCAAGGTTCTAGAAGACGATTAAGGGAAGGTCGTTCT
 CAGTGAAGAAATCAAAAAACAGAAAAAATGTTTATACAAACCTAAGTCAATAACCTGACCTTGAAGAAATTTGTA
 GAGCCAAAGTTGACTTCAGGAATGAACATCAGCACAAAGAGCAATCATCAAAATTTCTGACACAAATTTA
 ATATTTTTTTTTCTGATGAGAAACATGAGGGAAATTTGFGAGTTAGCCTCCTGTGGTAAAGGAATTTGAAGAAA
 ATATAACACCTTACACCTTTTTTCACTTTGACATTAAGATTTCTGGCTAACTTTGGAATCCATTAGAGAAAAAT
 CCTGTGACACAGATTCAATACAAATCAAAATGAGAGTTGTGAACCTGTATCCATTGAAAGACCGAGCCTTG
 TATGTATGTTATGGATACATAAAATGCCAGCAAGCCATTATCTCTCCATGGGAGCTAAGTTATAAAAATAGGT
 GCTTGGGTACAAAACTTTTTATATCAAAAGGCTTTGCACATTTCTATATGAGTGGGTTTACTGGTAAATATG
 TTATTTTTTACAACTAATTTTGTACTCTCAGAAATGTTTGTATATGCTTCTTGAATGCTATTTTAAATCTC
 AAACGTTTCAATAAAACCATTTTTTCAGATATAAAGAGAAATTACTTCAATTTGAGTAATTCAGAAAACTCAAGA
 TTTAAGTTAAAAAGTGGTTTGGACTTGGGAA

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FIGURE 42

CCCTTGAGACTCAAGATGATTCCCTTTTACCCATGTTTTCTCTACTATTGCTGCTTATTGTTAACCCCTATAAA
 CGCCAAACAAATCATTATGACAAGATCTTGGCTCATAGTCGTATCAGGGGTGGGACCAAGGCCCAATGTCTGTG
 CCCTTCAACAGATTTTGGGCACCAAAAAGAAATACTTCAGCACTTGTAAGAACTGGTATAAAAAGTCCATCTGT
 GGACAGAAAACGACTGTGTATATGAATGTTGCCCTGGTTATATGAGAATGGAAGGAATGAAAGGCTGCCGAGC
 AGTTTTGCCCATTGACCATGTTTATGGCACTCTGGGCATCTGGGASCCACCACACGACAGGCTTCTCTGAGC
 CCTCAAAACTGAGGGAGGAGATCGAGGGAAAGGGATCCTTCACCTACTTTGCACCGAGTAATGAGGCTTGGGAC
 AACTTGGATTCTGATATCCGTAGAGGTTTGGAGAGCAACGTGAATGTTGAATTACTGAATGCTTTACATAGTCA
 CATGATTAAFAAGAGAATGTTGACCAAGGACTTAAAAAATGGCATGATTATTCCTTCAATGTATAACAATTTGG
 GGCTTTTCATTAACCAATTATCCTAATGGGGTTGTCACTGTTAATTGTCTCGAATCATCCATGGGAACCAATTT
 GCAACAAATGGTGTGTCCATGTCTATTGACCGTGTGCTTACACAAATTTGGTACCTCAATTCAGACTTCATTGA
 AGCAGAAGATGACCTTTTCATCTTTAGAGCAGCTGCCATCACATCGGACATATTGGAGGCCCTTGGAGAGACG
 GTCACCTTCACACTCTTTGCTCCACCAATGAGGCTTTTGAGAACTTCCACGAGGTGTCTAGAAAGSATCATG
 GGAGACAAAGTGGCTTCCGAAGCTCTTATGAAGTACCACATCTTAAATACCTCTCCAGTGTCTGAGTCTATTAT
 GGGAGGAGCAGTCTTTGACACGCTGGAAGGAATFACAAATGAGATAGGATGTGACGGTGACAGTATAACAGTAA
 ATGGAATCAAAATGGTGAACAAAAGGATATTGTGACAAATAATGGTGTGATCCATTTGATTGATCAGGTCCCTA
 ATTCTGTATTCTGCCAAACAAAGTTATTGAGCTGGCTGGAAACAGCAACACCTTCACGGATCTTGTGGCCCA
 ATTAGGCTTGGCATCTGCTCTGAGGCCAGATGGAGAATACACTTTGCTGGCACCTGTGAATAATGCATTTTCTG
 ATGATACTCTCAGCATGGATCAGCGCCTCCTTAATTTAATTCTGACAGATCACATATTGAAGTAAAAATTGGC
 CTTAATGASCTTTACACGGCCAAATACTGGAAACCATCGGAGGCCAAACAGCTCAGAGTCTTGTATATCGTAC
 AGCTGTCTGCATTGAAAATTCATGCTGGGGAAGGGAGTAAGCAAGGGAGAAACGGTGGCAATTCACATATTCC
 GCGAGATCATCAAGCCAGCAGAGAAATCCCTCCATGAAAAGTTAAAACAAGATAAGCGCTTTAGCACCTTCCTC
 AGCCTACTTGAAGCTGCAGACTTGAAAGAGCTCCTGACACAACCTGGAGACTGGACATTAFTTGTGCCAACCAA
 TGATGCTTTTAAGGGAATGACTAGTGAAGAAAAAGAAATTCGTATCGGACAAAAATGCTCTTCAAAACATCA
 TTCCTTATCACCTGACACCAGGAGTTTTCATTGGAAAAGGATTTGAACCTGGTGTACTAACATTTTAAAGACC
 ACACAAAGGAAGCAAAATCTTTCTGAAAGAGTAATGTACACTTCTGCTGATGAATTGAATCBAAGAAATC
 TGACATCATGACAACAAATGGTGTATTCATGTTGTAGATAAACTCCCTCTATCCAGCAGACACACCTGTTGGAA
 ATGATCAACTGCTGGAAATACTTAATAAATTAATCAAATACATCCAAATTAAGTTTGTTCGTGCTAGCACTTC
 AAAGAAATCCCCGTGACTGTCTATAGACCCACACTAACBAAAGTCAAAATGAAGGTGAACCTGAATTCAGACT
 GATTAAAGAGGTGAAACAATAACTGAAGTGATCCATGGAGAGCCAAATTAATAAAAAATACACCAAAATCATTG
 ATGGAGTGCCTGTGGAAATAACTGAAAAAGAGACACGGAAGAAGCAATCATTACAGGTCTGAAATAAATAC
 ACTAGGATTTCTACTGGAGGTGAGAAACAGAAAGAACTCTGAGGAATTTGTACAAGAAGAGGTACCAAGGT
 CACCAAAATTCATTGAAGGTGGTGTGTTGTTTATTTGAAGATGAAGAAATTAAGAACTGCTTCAGGGAGACA
 CACCCGTGAGGAAGTTGCAAGCCACAAAAAGTTCAAGGATCTAGAGACGATTAAGGGAGGCTGTTCTCAG
 TGAAGGGC

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FIGURE 43

CCGTTGAGACTCAAGATGATTCCCTTTTACCCATGTTTTCTCTACTATTGCTGCTTATTGTTAACCCCTATAAA
 CGCCAAACAATCATTATGACAAGATCTTGGCTCATAGTCGTATCAGGGGTGGGGACCAAGGCCCAATGCTGTG
 CCCTTCAACAGATTTTGGGCACCAAAAAGAAATCTTCAGCACTTGTAAAGACTGGTATAAAAAGTCCATCTGT
 GGACAGAAAACGACTGTGTTATATGAATGTTGCCCTGGTTATATGAGAATGGAAGGAATGAAAGGCTGCCAGC
 AGTTTTGCCCATGACCATGTTTATGGCACTCTGGGCATCGTGGGAGCCACCACAACGAGGCTATTCTGACG
 CCTCAAAACTGAGGGAGGAGATCGAGGGAAAGGGATCCTTCACTTACTTTGCACCGAGTAATGAGGCTGGGAC
 AACTTGGATTCTGATATCCGTAGAGGTTTGGAGAGCAACGTGAATGTTGAATTACTGAATGCTTTACATAGTCA
 CATGATTAATAAGAGAATGTTGACCAAGGACTTAAAAAATGGCATGATTAATTCCTTCAATGTATAACAATTTGG
 GGCTTTTCATTAAACCATATCCTAATGGGTTTGTCACTGTTAATTGTGCTCGAATCATCCATGGGAACAGATT
 GCAACAAATGGTGTGTGCCATGTCATTGACCGTGTGCTTACACAAATTTGGTACCTCAATTCAGACTTCATTGA
 AGCAGAAAGATGACCTTTCATCTTTTAGAGCAGCTGCCATCACATCGGACATATTGGAGGCCCTTGGAGAGACG
 GTCACCTTCACTCTTTTCTCCACCAATGAGGCTTTTGAGAACTTCCACGAGGTGTCTAGAAAAGGATCATG
 GGAGACAAAGTGGCTTCCGAAGCTCTTATGAAGTACCACATCTTAATACTCTCCAGTGTCTGAGTCTATTAAT
 GGGAGGAGCAGTCTTTGAGAGCTGGAAGGAATACAAATTGAGATAGGATGTGACGGTGCAGTATAACAGTAA
 ATGGCAATCRAAATGTTGAACAAAAAGGATATTGTGACAAATAATGGTGTGATCCATTTGATTGATCAGGTCTTA
 ATTCCCTGATTCTGCCAAACAAGTTATTGAGCTGGCTGGAAACAGCAAAACCACCTTCACGGATCTTGTGGCCCA
 ATTAGGCTTGGCATCTGCTCTGAGGUCAGATGGAGAAATACACTTTGCTGGCACCTGTGAATAATGCATTTCTG
 ATGATACTCTCAGCATGGATCAGCGCTCCTTAATTAATTTCTGAGAAATCACATATTTGAAACTAAAAGTTGGC
 CTTAATGAGCTTTACACGGGCAATACTGGAAACCATCGGAGGCRAACAGCTCAGAGTCTTCGTATATCGTAC
 AGCTSTCTGCATTTGAAATTCATGCATGGAGAAAGGGAGTAAGCAAGGGAGAAACGGTGGCATTCACATATTCC
 CGGAGATCATCAAGCCAGCAGAGAAATCCCTCCATGAAAAGTTAAAACAAGATAAGCGCTTTAGCACCTTCCCTC
 AGCCTACTTGAAGCTGCAGACTTGAAAGAGCTCCTEACACACCTGGAGACTGGACATTAATTTGTGCCAACCRA
 TGATGCTTTTAAGGSAATGACTAGTGAAGAAAAAGAAATTTCTGATACGGGACAAAAATGCTCTTCAAAACATCA
 TTCTTTATCACCTGACACCCAGGAGTTTTCATTGGAAAAGGATTTGAACCTGGTGTACTAACATTTTAAGACC
 ACACAAGGAAGCAAAATCTTTCTGAAAGAAGTAAATGATACACTTCTGGTGAATGAATTGAAATCAAAAGAATC
 TGACATCATGACACAAATGGTGTAAATTCATGTTGTAGATAAACTCCTCTATCCAGCAGACACACCTGTTGGAA
 ATGATCAACTGCTGSAATTAATAAATTAATCAATACATCCAAATTAAGTTTGTTCGTGGTAGCACCTTC
 AAAGAAATCCCGTGACTGTCTATAAGCCATTATTAAAAAATACACCAAAATCATTGATGAGTGCCTGTGGGA
 AATAACTGAAAAGAGACACGAGAGAAGCAATCATACAGGTCTGAAATAAAATACACTAGGATTTCTACTG
 GACGTGGAGAAACAGAGAAACTCTGAAGAAATTTGTACAGAAAGACACACCCGTGAGGAAAGTTGCAAGCCAAC
 AAAAAAGTTCAAGGATCTAGAAGACGATTAAGGGAAGGTCCTTCTCAGTGAAGGGC

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FIGURE 44

CCCTTGAGACTCAAGATGATTCCCTTTTACCCATGTTTTCTCTACTATTGCTGCTTATTGTTAACCCTATAAA
 CGCCAACAATCATTATGACAGATCTTGGCTCATAGTCGTATCAGGGGTCGGGACCAAGGCCCAAATGTCTGTG
 CCCTTCAACAGATTTTGGGCACCAAAAAGAAATACTTCAGCACTTGTAAAGACTGGTATAAAAAGTCCATCTGT
 GGACAGAAAACGACTGTGTATATGAATGTTGCCCTGGTTATATGAGATGGAAGGAATGAAAGGCTGCCCAGC
 AGTTTTGCCCATTGACCATGTTTATGGCACTCTGGGCATGCTGGGASCCACCACAACGCGAGCGCTATTCTGACC
 CCTCAAAACTGAGGGAGGAGATCGAGGGAAAGGGATCCTTCACCTTACTTTGCACCGAGTAATGAGGCTTGGGAC
 AACTTGGATTCTGTATATCCGTAGAGCTTTGGAGAGCAACGTGAATGTTGAATTACTGAATGCTTTACATAGTCA
 CATGATTAATAAGAGAATGTTGAACCAAGGACTTAAAAAATGGCATGATTATTCCCTCAATGTATAACAATTTGG
 GGCTTTTCATTAACCATTTATCCTAATGGGGTTGTCACTGTTAATTTGTGCTCGAATCATCCATGGGAACAGATT
 GCAACAAATGGTGTGTCCATGTCTATTGACCGTGTGCTTACACAAATPGGTACCTCAATTCAAGACTTCATTGA
 AGCAGAGATGACCTTTTATCTTTTAGAGCAGCTGCCATCACATCGGACATATTGGAGGGCCCTTGGAGAGACG
 GTCACCTTCACACTCTTTGCTCCCAATGAGGCTTTTGAGAAACTTCCACGAGGTGTCTAGAAAGGATCATG
 GGAGACAAAGTGGCTTCCGAAGCTCTTATGAAGTACCACATCTTAATACCTCCAGTGTCTGAGTCTATTAT
 GGGAGGAGCACTCTTTGAGACGCTGGAAGGAATACAAATGAGATAGGATGTGAACGCTGACAGTATAACAGTAA
 ATGGAATCABAATGGTGAACAAAAGGATATTGTGACAAATAATGGTGTGATCCATTTGATTGATCAGGTCCTA
 ATTCTGATTCTGCCAAACAAGTTATTGAGCTGGCTGGAAAACAGCAAAACCACCTTCACGGATCTTGTGGCCCA
 ATTAGGCTTGGCATCTGCTCTGAGGCCAGATGGAGAAATACACTTTGCTGGCACCCTGTGAATATATCATTTTCTG
 ATGATACTCTCAGCATGATCAGCGCTCCTTAAATTAATTTCTGCAGAATCACATATTGAAAGTAAAGTTGGC
 CTTAATGAGCTTTTACAACGGGCAATACTGGAAACCATCGGAGGCCAAACAGCTCAGAGTCTTCGTATATCGTAC
 AGCTGTCTGCATTCABAATTCATGCTATGGAGAAAGGAGTAAGCAAGGGAGAAACGGTSCGATTACATATTC
 GCGAGATCATCAAGCCAGCAGASAAATCCCTCCATGAAAATTTAAAAACAAGATAGCGCTTTAGCACCTTCCTC
 AGCCTACTTGAAGCTGCAGACTTGAAGAGGCTCCTGACACAACCTGGAGACTGGACATTATTTGTGCCAACCAA
 TGATGCTTTTBAAGGAATGACTAGTGAAGAAAAGAAATTTCTGATACGGGACAAAATGCTCTTCAAAACATCA
 TTCTTTATACCTGACACACAGGACTTTTCATTGGAAAAGSATTTGAACCTGGTGTACTAACAATTTTAAAGACC
 ACACAAGGAAGCAAAATCTTTCTGAAAGAAGTAATGTATACACTTCTGGTGAATGAATTGAAATCAAAAGAATC
 TGACATCATGACAACAAATGGTGTAAATTCATGTTGTAGATAAACTCCTCTATCCAGCAGACACACCTGTTGGAA
 ATGATCAACTGCTGGAAATACTTAATAAAATTAATCAATACATCCAAATTAAGTTTGTTCGTGGTAGCACCTTC
 AAAGAATCCCGTGACTGTCTATAGACCCACACTACAAAAGTCAAAATTGAAGGTGAACCTGAATTCAGACT
 GATTAAAGAGGTGAACAATACTGAAGTGAATCCATGGAGAGCCAATTATTAAAAAATACACCAAAATCATTG
 ATGGAGTGCTGTGGAATAACTGAAAAAGAGACACGAGAGAACGAATCATTACAGGTCTGAAATAAATAC
 ACTAGGATTTCTACTGGAGGTGGAGAAACAGAAAGAACTCTGAAGAAATTTGTACAAGAAGACACACCGGTGAG
 GAAGTTGCAAGCCAAACAAAAAGTTCAAGGATCTAGAGACGATTAGGGAGGTCGTTCTCAGTGAAGGGC

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FIGURE 45

CCCTTSAGACTCAAGATGATTCCCTTTTACCCATGTTTTCTCTACTATTGCTGCTTATTGTTAACCCTATAAA
 CGCCAAACAATCATTATGACAAGATCTTGGCTCATAGTCGTATCAGGGGTCCGGACCAAGGCCCAAATGCTCTGTG
 CCGTTCAACAGATTTTGGGACCCAAAAGAAATACTTCAGCACTTGTAAGAACTGGTATAAARAGFCCATCTGT
 GGACAGAAAACGACTGTGTTATATGAATGTTGCCCTGGTTATATGAGAATGGAAGGAATGAAAGGCTGCCCCAGC
 AGTTTTGCCCCATGACCATGTTTATGSCACTCTGGGCATCGTGGGAGCCACCACACGCGAGCGCTATTCTGACG
 CCTCAAAACTGAGCGGAGGAGATCGAGGGAAGGGATCCTTCACTTACTTTGCACCGAGTAATGAGGCTTGGGAC
 AACTTGGATTCTGAATCCCGTAGAGGTTTGGAGAGCAACGTGAATGTTGAATFACTGAATGCTTTACATAGTCA
 CATGATTAATAAGAGAATGTTGACCAAGGACTTAAAAAATGGCATGATTATTCTTCAATGTATAACAATTTGG
 GGCTTTTCATTAACCAATATCCTAATGGGGTTGTCACCTTTAATTGCTCGAATCATCCATGGGAACAGATT
 GCAACAAATGGTGTGTCATGTCTTGAACCTGTGCTTACACAAATTGGTACCTCAATTCAAGACTTCATTGA
 AGCAGAAGATGACCTTTCATCTTTTAGAGCAGCTGCCATCACATCGGACATATTGGAGGGCCCTTGGAAAGAGACG
 GTCACCTTACACTCTTTGCTCCCAACATGAGGCTTTTGAGAAACTTCCACGAGGTGTCTTAGAAAGGATCATG
 GGAGACAAAGTGGCTTCCGAAGCTCTTATGAAGTACCACATCTTAAATACTCTCCAGTGTCTGAGTCTATTAT
 GGGAGGAGCAGTCTTTGAGACGCTGGAAAGGAATACAAATTGAGATAGCATGTGACGGTGCAGATATAACAGTAA
 ATGGAATCAAAATGCTGAACAAAAGGATATTGTGACAAATAATGGTGTGATCCATTGATTGATCAGGTCTTA
 ATTCTGATTCTGCCAAACAAGTTATTGAGCTGGCTGGABACAGCAAACACCTTCACGGATCTGTGAGGCCA
 ATTAGGCTTGGCATCTGCTCTGAGGCCAGATGGAGAATACACTTTGCTGGCACCTGTGAATTAATGCATTTTCTG
 ATGATACTCTCAGCATGGATCAGCGCTCTTAAATTAATCTGCAGAAATCACATATTGAAGTAAAGTGGC
 CTTAATGAGCTTTACAACGGGCAATACTGGAAACCATCGGAGGCCAAACAGCTCAGAGTCTTGGTATATCGTAC
 AGCTGTCTGCATTGAAAATTCATGCATGGAGAAAGGGAGTAAGCAAGGGAGAAACGGTGGGATTACATATTCC
 GCGAGATCATCAAGCCAGCAGAGAAATCCCTCCATGAAAAGTTAAACACAGATAAGCGCTTTAGCACCTTCCTC
 AGCCTACTTGAAGCTGCAGACTTGAAGAGCTCCTGACACAACCTGGGAGACTGGACATTAATTTGTGCCAACCA
 TGATGCTTTTAAGGGAATGACTAGTGAAGAAAAAGAAATTTCTGATACGGGACAAAATGCTCTTCAAAACATCA
 TTCTTTATCACCTGACACCAGGAGTTTTCAATTGAAAAGGATTTGAACCTGGTGTACTAACATTTTAAGAGCC
 ACACAAGGAAGCAAAATCTTTCTGAAGAGAGTAAATGATACACTTCTGGTGAATGAATTGAATCAAAAGAAATC
 TGACATCATGACACAAATGGTGTAAATTCATGTTGTAGATAAACTCCTCTATCCAGCAGACACCTGTGGA
 ATGATCAACTGCTGGAATACTTAATAAATTAATCAAAATACATCCAAATTAAGTTTGTTCGTGGTAGCACCTTC
 AAAGAAATCCCCGTGACTGTCTATAGCCAATTATTAAAAAATACACCAAAATCATTGATGGAGTGCCTGTGGA
 AATAACTGAAAAAGAGACACGAGAGAAGAACCAATCATTACAGGTCCTGAAATAAATACACTAGGATTTCTACTG
 GAGGTGGAGAAACAGAGAAACTCTGAAGAAATTTGTTACAAGAAGAGGTCAACCAAGGTCACCAAAATTCATTGAA
 GGTGGTGAATGCTCAATTTATTTGAAGATGAAGAAATTAAGAGACTGCTTCAGGGAGACACACCCGTGAGGAAGTT
 GCAAGCCACAAAAAAGTTCAAGGATCTAGAGAGCGATTAAAGGAAGGTCGTTCTCAGTGAAGGGC

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FIGURE 46

ACACGGACCAAGGAGTCTAACACGTGCGCGAGTCCGGGGCTCGCACGAAAGCCGCGTGGCGCAATGAAGGTGA
 AGGCCGGCGCGCTCGCCGGCCGAGGTGGGATCCCGAGGCCTCTCCAGTCCGCCGAGGGCGCACCCGSCCCGT
 CTGCCCCGCCCGCGCCGGGGAGGTGGAGCACGAGCGCACGTGTTAGGACCCGAAAGATGGTGAACATATGCTGGG
 CAGGGCGAASCCAGAGGAAACTCTGGTGGAGGTCCGTAGCGGTCTTGACGTGCAAAATCGGTCCGTCCGACCTGGG
 TATAGGGGCGCGCTCCAGGCGAGGCGGTGGAGCGCTCCGTGAAACTTGCSCGCGCGCTCGCGCCACTGCGCCCGG
 AGCGATGAAGATGGTCCGCGCCCTGGACGCGGTCTACTCCAACAGCTGCTGCTTGCTGCTGCCATGTCCGACCCG
 GCACCATCTCTGCTCGCGCTCTGGTATCTGATCATCAATGCTGTGGTACTGTTGATTTTATTGAGTGCCCTGGCT
 GATCCGGATCAGTATTAACATTTCAAGTCTGAACTGGGAGGTGACTTTGAGTTCATGGATGATGCCAACATGTG
 CATTGCCATTGCGAATTTCTCTCTCATGATCCTGATATGTGCTATGGCTACTTACGGAGCGTACAAGCAACGCG
 CAGCCTGGATCATCCCATTTCTCTGTTACCAGATCTTTGACTTTGCCCTGAACATGTTGGTTCGAATCACTGTG
 CTTATTTATCCAACTCCATTCAGGAATACATACGGCAACTGCCTCCTAATTTTCCCTACAGAGATGATGTCTAT
 GTCAGTGAATCCTACCTGTTTGGTCTTATTTATTTCTCTGTTTATTAGCATTATCTTGACTTTTAAGGGTTACT
 TGATTAGCTGTGTTTGGAACTGCTACCGATACATCAATGCTAGCAACTCCTCTGATGTCTGCTTTATGTTACC
 AGCAATGACACTACGGTGTGCTACCCCCGTATGATGATGCCACTGTGAATGGTGTGCTGCCAAGSAGCCACCGCC
 ACCTTACCTGTCTGCCGTAAGCCTTCAAGTGGGCGGAGCTGAGGGCAGCAGCTTGACTTTGCAGACATCTGAGCA
 ATAGTTCTGTTATTTCACTTTTGGCCATGAGCCTCTCTGAGCTTGTTTGTGCTGAAATGCTACTTTTAAATTT
 TAGATGTTAGATTGAAAACGTAGTTTTCAACATATGCTTTGCTAGAACACTGTGATAGATTAACTGTAGAATT
 CTCTCTGTACGATTGGGGATATATAGGGCTTCACTAACCTTCCCTAGGCATTGAAACTTCCCCCAAATCTGATG
 GACCTAGAACTCTGCTTTTGTACCTGCTGGGCCCCAAAGTGGGCAATTTTCTCTCTGTTCCCTCTCTTTTGA
 AATGTAAATAAAACCAAAATAGACAACCTTTTCTTCAGCCATTCACCATAGAGAACAAACCTTATGGAAA
 CAGGAATGTCAATTGTGTAATCATTTGTTCTAATTAGGTAAATAGAACTCCTTATGTATGTGTTACAAGAAATTC
 CCCCACAACATCTTTTATGACTGAAGTTCAATGACAGTTTGTGTTGGGTGGTAAAGGATTTTCTCCATGGCCT
 GAATTAAGACCATTAGAAAGCACCAGGCGGTGGGAGCAGTGACCATCTGCTGACTGTTCTTGTGGATCTTGTGT
 CCAGGGACATGGGGTGACATGCCTCGTATGTGTTAGAGGGTGAATGGATGTGTTTGGCCTGCATGGGATCTG
 GTGCCCCCTCTCTCTCTGATTACATCCCCACCCAGGGCCCGCTTTTACTAAGTGTCTGCCCTAGATTGGTTC
 AAGGAGGTCTATCCAAGTACTTTATCAAGTGAATTTGGGATATATTTGATTAFACTTCTGCCCTAACACATGGAA
 AAGGTTTTTCTTTTCCCTGCAAGCTACATCCTACTGCTTTGAACTTCCAAGTATGTCTAGTCACTTTTAAAT
 GTAAACATTTTCAGAAAATGAGGATTCCTTCTCTGTATGCGCTTTTACCTTGACTACCTGAATGCAAGGG
 ATTTTTATATATTCATATGTTACAAAGTCAGCAACTCTCCTGTTGGTTCATTTATTGAATGTGCTGTAAATTAAG
 TTGTTTGCATTAACACAGGTTTCCCCACAAAAA

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FIGURE 47

ATTTCGCCCTTCGAAAGATGGTGAACTATGCCTGGGCAGGGCGGGCTCCAGGCGAGGCGGTCGACGCTCCTGAA
AACTTGCGGCGCGCGCTCGCGCCACTGCGCCCGAGCGGATGAAGATGGTCGCGCCCTGGACTCGGTTCTACTCCA
ACAGCTGCTGCTTGTGCTGCCATGTCCGACCCGGCACCATCCTGCTCGGCCTCTGGTATCTGATCATCAATGCT
GTGGTACTGTGATTTTATTGAGTGCCCTGGCTGATCCGGATCAGTATAACTTTTCAAGTTCTGAACTGGGAGG
TGACTTTGAGTTCATGGATGATGCCAACATGTGCATTGCCATTGCGATTTCTCTTCTCATGATCCTGATATGTG
CYATGGCTACTTACCGAGCGTACAAGCAACGCGCAGCCTGGATCATCCCATTCTTCTGTATACGATCTTTGAC
TTTCCCTGAACATGTTGGTTGCAATCACTGTGCTTATTTATCCAACTCCATTCAGGAATACATACGGCAACT
GCCTCCTAATTTTCCCTACAGAGATGATGTGATGTGAGTGAATCCTACCTGTTTGGTCTTATTATTCTTCGT
TTATTAGCATTATCTTGACTTTTAAAGGGTTACTTGATTAGCTGTGTTTGGAACTGCTACCGATACATCAATGGT
AGGAATCCTCTGATGTCTGTTTATGTTACCAGCAATGACACTACGGTGTGCTACCCCGTATGATGATGC
CACTGTGAATGGTGTCTGCCAAGGAGCCACCGCCACCTTACCTGTCTGCCTAAGCCTTCAATGGGCGGAGCTGA
GGCCAGCAGCTTGACTTTCAGACATCTGAGAAGGGC

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FIGURE 48

AGCGCCCATGEGGGCGAGCCCGGGGGCGGGGGCCCGGGCCCGGGCCCGCCGCTGCTGCTGTTTCTGGGGGCGCG
 GCTGGTCTCTGGCTCTGSSGCGCTGCCGGCGCGTGAGGCGGGCAGCGCGSTTGAGGCGGAAGAGCTGGTGAAGG
 GCAGCCCCGGCGTGGGAGCCGCTGCCAAGCACACGCGGGAGAGAGCCCGCCCCACAGCGGCTGGGGAGATGAG
 GCGTCTGPGGACGGCGCCCGSTGGCGAGCTGGCCGGGCCAGAGAGGTTGCTGCAGGAGTGGGCTGGCGTGACCGG
 CACCGCTGGCTGGAGCTGACAGCCAGGCTGGGAGGAGTGACCGCAGAGGCGGGCAGCGCGGATGCCAGG
 CCGTCCAGCTACGCTCCAGGCTCCCCAGAGGTTCTCGGGCAGTCAATCATGCCCCCTGCCATTCCTGAGGCT
 ACAGAGGCCAGCGGGGCCACCCCTCCCCACCCCCGGCGACAAGCTGAGCCCCAGCTTCTGAATCCCCAAGGAGAG
 CCCCTTGGAGGTTTGGCTGAACCTGGGGGGCAGCACACCCGACCCCTCAAGTGCCAGAGCTGACTTACCCATTTC
 AGGGCACCCCTGGAGCCCCAACCGGATCAGATATCATTTGACATCGACTACTTCSAAGGAGTGGATGCTGAGGGT
 CGTGGCGCAGATCTGGGGAGCTTCCAGAGGTCACCAGGAACCTCAGAGAACCCCTGATACTGAGGGAGAGAC
 CCGTCCCTGGAGCCTGCTTGACTTATACGATGATTTACCCCCCTTCGATGAATCTGATTTCTACCCACCCACAT
 CCTTTTATGATGACTTGGATGAAGAGGAGGAGGAAGAGGAGGATGACAAAGATGCCAGTAGGAGGTGGAGACCTA
 GAAGATGAAATGAGCTTCTAGTCCCCACTGGGAAGCCTGGTCTGGGGCCCGGGACAGGCCAGCCACCACTCG
 GTGGCATGCTCTCCCTCCACAGCACACTCTGGGCTCGGTCCCCGGCAGCAGCATCGCCCTCAGGCCCCGCCAG
 GAGAGCCAGGCGGGACTTGGCCCTCCAGTGAAATGGCACTGAGTGCCGCACTGGCTTTGTGGGGCATAACGGC
 TCCTGCCGCTCAGTGTGCGACCTCTTCCCAAGTTACTGTCACAATGGCGGCCAGTCTACCTGGTGGAGAACAT
 AGGGGCCCTTCTGCAGCTGCAACACGAGGACTACATCTGGCACAAGGGGATGCGCTGGAGTCCATCATCACCG
 ACTTCCAGGTGATGTGCGTGGCCGTGGGCTCGGCTGCGCTCTGCTCTCTGCTCTTCATGATGACGCTGTTC
 TTTGCCAAGAAGCTCTACCTGCTCAAGACGGAGAATACCAAGCTGCGTAGGACCAACAAATTCGGGACCCCATC
 TGAGCTCCACAATGATAACTTCTCCCTCTCCACCATTCGCGAGGGCTCTCACCCAAATGATGATCCTAGTGTCT
 CCCACAANAATCCAGGAGGTTCTCAAGTCTGCTGAAAGAGGAGGAGTCAATTAACATCCAGAACTCCATGTCTG
 CCCAAACTTGAGGGTGGCAAGGTGACAGGCTGACTTGGATGTGAATGTCTTTCAGAATAATTTAACTAAG
 CAGAGCAGAGAGAGAGGAGCGCGCTAGTGGGTGGGGGTAGGGAGAAACATTTATCTCTCTTGTACAGAGTCT
 ATTTCTTGTAAACATTTGTTAACTC

[illegible]

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FIGURE 50

CTCCTGCCAGGGGAGAGAGAGGCGTCTGCAGGGGGCAGAGACCGCAGCTACCTGCCGGGTGGGCCCCCCAC
 CCAGGAGCGCTCGCTTCGCCCCCTTTCTCCCCCCCCCCCCACCTCCTTATTGGTGCCTAGTTTGCAGCGCCACG
 CTCTTGGCGCTTCGCTTCGGCTTTGAATCTGGCTCGCCCCCTTCGTATTATGCTCTGCACTCCGAAGGAAATTTGG
 GGACGATTATCAGGTAGTGACCATCCTCCAGCGGCTCGGGCTTGCAGCCCCAGGGGGCCAGGCCAGGACCTTC
 AGCAGCAGCTTGTGCCCAAGAGAGCGGGCAGCGGCTTCTGGACAAGAACGGCCGGTGCATGTACAGCACGGC
 AACCTGGGCAGCGAGACAAGCCGCTACCTCTCGGACCTCTTCACCACGCTGGTGGACCTCAAGTGGCGCTGGAA
 CCTCTTCATCTTCATTCTCACCTACACCGTGGCGCTGGCTTTTCNIGGCGTCCATGTGGTGGGTGATCGCCTACA
 CTCGGGGGGCAGCTGAACAAAGCCCCACGTCGGTAACACAGCCCTTGGCTGGCCAATGTCTATAACTTCCCTTCT
 GCCTTCCTCTCTTCATCGAGACGGAGGCCACCATCGGCTATGGCTACCGATACATCACAGACAAGTGGCCCCA
 GGGCATCATCTCTCTCTCTCCASTCCATCCTGGGCTCCATCGTGGACGCTTCCTCATCGGCTGCATGTTC
 TCAAGATGTCCAGCCCCAAGAGCGCGCCGAGACCTCATGTYCAGCGAGCACGGCGTGTCTCCATGAGGGAC
 GGAAAACTCACGCTTATGTTCCGGGTGGGCAACCTGCGCAACAGCCACATGGTCTCCGCGCAGATTCCGTGCAA
 GCTGCTCAATCTCGGCAGACACCTGAGGCTGAGTTCCCTCCCTTGACCACTTGAAGTGGATGTAGGTTTGA
 GTACAGGGGGCAGATCAACTTTTTCTGTGTCCCCCTCACAATTTGCCACGTGATCGATGCCAAGGCCCTTT
 TATGACCTATCCAGCGAGCATGCAAACTGAACAGTTTCGAGATTGTCTCATTCCTAGAGGGCATTGTGGAAAC
 AACTGGGATGACTTGTCAAGCTCGAACATCTATFACTGAAGATGAAGTCTTTGGGGTCATCGTTTTTTCTCTG
 TAATTTCTTAGAAGAGGGATTCTTTAAAGTTGATTACTCCAGTTCCACGCAACATTTGAAGTCCCCACCCCA
 CCTTACAGTGTGAAAGAGCAGGAGGAATGCTTCTCATGTGCTCCCTTTAATAGCACCCAGCCATAACTACAG
 CAAAGAAAGACATAAATCTGTGGAAATGCTTAGATGGACTAGATGATATTACTACAAACTACCATCTAAGCTGC
 AGAAAATTACTGGAGAGAGAGCTTTCCCAAAAACCTCTTGAGGATGAGTCTACAACTTCAGAAAAGCCCTAC
 AGCTTGGGAGACTTGGCCATGAAACTTCAACGAATAAGTTCAAGTTCCGGGCAACTCAGAGGAAAACTGGTATC
 TAAAACCAACAGATGTTATCTGATCCCATGAGCCAGTCTGTGGCTGATTTGCCACCAAGCTTCAAAAGATGG
 CTCGGAGGAGCAGCTAGGATGGAAGGGAACCTTCCAGCCAAATTAAGCAAAATGAACTCTGATCGCTTCACATAA
 CAAAGCACTCCCTTAGGCATTATTTAATGTTTGAATTTAGTAATAGTCCAATATTTGGCGATGAGGTAATTTCTC
 CTAAGGAATCTGAAAGTATATTTCTCTCCAGTTCTACAGCATATTTGAGAGACCTTCTCTTCCCAAGTATTG
 CGAATGTGCAGAAAGCAACAGTTACGGAGGGGAGGACATCATAGGAAGTTATTAACGGGCATGTATATACAT
 CAGGCTGCAATAATGTGCAATTTTGCATTTAGTTTATGGCATGATTTATATATGGCATTTTATATTGTAT
 ATTCTGGAAAAAATATATATATATATATTTAAAGGGGAGATACTCTCCCTGACATTTCTAACATATGTATTAA
 GCCAACATGAGTGAATAGCTTTCAGGGCGATAAAAACTAATATATGTCTGTGTGTGTGTGTATGTATACAC
 ATATATACATATATATATACATACATACATACATACATACATATATATCTGATAAAATTTGTATGT
 TTTGTTCAAAGTTGTAGTTCTTGTGCATGTTTACTTTATTAGAGTAGGAGGCTACTGGCATTAAATTAATA
 CCAATATTTTTCGCTTAATTTTGTCTATTTTAAATCTGATTTAATGTTTCTGCTGTTTAAAGTCTTGGGA
 GGCTTTCAATTTGTATTTTATATGAGAGAAATCACACAAGTTTGTGCTATCTATGGCCCTGCAAAATATAACCAT
 TACATGTTTAAATTTGTAATTTTAGAGCATACAGTACTCAGTATAGCATTGAACATTTCTTATGATTTTAA
 AGTTGCTAGTACTGGGAGAAATAATTTGTGATTAATTTGAGAATTAATTCCTTTCTAGACTAATTAATCTG
 GAAATCTGTTTGTATATGATCTAATACAAAGATCAGCTCTGAACAACACTGAATCATGTTAATAGACAGTAG
 CCAAGTTATATTGAATATATCAGAACTCTGTGTGAAGTTACACAATTAATTTCTGTTTCAAAGTGAATTAAT
 TGGAAACATTTTCTTCTTTTCTGGAAATTTTGTCCATTTTAAAAACCAATCATTTTAAAGAGACATGCAAT
 GCAATGAAACAGATGTAATATTTATGCTTAAATTAATAAAAAAAAAA

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FIGURE 51

GAGAGGGTCTCTTCAGGGGCTGCTTATG000CTTGTTCAAGAACACACAGTGTACAGCTCTCTGTACTCTGGTTGCAG
 ACTGACCTTGCTCAGG0CTGAGAAAGGATGGGGCAGG0CACCAGAGTGGATGCTGTCTGCACCCATCGTCTTGACC
 CCAAAAG000CTGGACTGGACAGAGAGCGGCTGTACTGGAGGCTGAGCCAGCTGACCCAGGGCATCACTGAGCTG
 GG000CTACAC0CTGGACAGGACAGTCTCTATGTCAATGGTTTCA00CATCAGAGCTCTATGAGGACCA0CAG
 AACTCTGTATACCTCCACAATGCACCTGGCA0CTGASAACTCCAG0CTCCCTGTCTGGACCTACGACCGCCA
 G00CTCTCCTGGTGTATTTACAAATTAACCTTCA0CATCACTAACCTGCGGTATGAGGAGAACATGCATCAC0CT
 GGCTCTAGAAAGTTTAA0CACCA0CGAGAGAGTCCCTTCAGGGTCTGCTCAGG0CTGTGTTCAAGAACACAGTGT
 TGG00CTCTGTACTCTGGCTGACAGTGTGCTCAGG0CCAAGAGGATGGGGCAG0CA0CAAAAGTGGATG
 CCATCTGCACCTACCG00CTGATCCCAAAAG00CTGGACTGGACAGAGAGCAGCTATACTGGGAGCTGAGCCAG
 CTAACCCACAGCATCACTGAGCTGGG000CTACAC0CTGGACAGGGACAGTCTCTATGTCAATGGTTTCA0CA
 GCGGAGCTCTGTGCCACCACTAGCATTCTGGGAC0000CACAGTGGACCTGGGAACATCTGGGACTCCAGTTT
 CTAAC0CTGGTCCCTCGGCTGCCAG00CTCTCCTGGTGTATTTCACTCTCAACTTCACCATCA0CAACCTGCGG
 TATGAGGAGAACATGACAGC00CTGGCTCCAGGAAGTTCAACACCA0CGAGAGGGTCCCTTCAGGG0CTGCTCAG
 GT000CTGTTCAAGAGCACCAGTGTGGG00CTCTGTACTCTGGCTGACAGTGTACTTTGCTCAGG0CTGAAAAGG
 ATGGGACAGCCACTGGAGTGGATGCCATCTGCACCCACCA0CTGACCCCAAAAG00CTAGGCTGGACAGAGAG
 CAGCTGTATTTGGGAGCTGAGCCAGCTGACCCACAATATCACTGAGCTGGG0CACTATG000CTGGACAACGACAG
 CCTCTTTGTCAATGGTTTCACTCACTGGAGCTCTGTGTCCACCA0CAGCACTCCTGGGAC0000CACAGTGTATC
 TGGGAGCATCTAGAGTCCAG0CTCGATATTTGG00CTTCAGCTGCCAGCCATCTCCTGATACTATTCA00CTC
 AACTTCACCATCACTAACTGCGGTATGAGGAGAACATGTGGCTGGCTCCAGGAAGTTCAACACTACAGAGAG
 GGTCTTCAGGG0CTGCTAAGG00CTTGTTCAAGAACACAGTGTGGG00CTCTGTACTCTGGCTCCAGGCTGA
 CCTGCTCAGG00CAGAGAAAGTGGGGAAGCCACCGAGTGGATGCCATCTGCAC00CAGG00CTGACCC0CA
 GG00CTGGGCTGGACAGAGAGCAGCTGTATTTGGAGCTGAG00CAGCTGACCCACAGCATCACTGAGCTGGG000
 CTACACACTGGACAGGACAGTCTCTATGTCAATGGTTTCA00CATCGGAGCTCTGTAC00CA0CAGCAG00
 GGGTGGTCAG0GAGGAGCCATTCACACTGA0CTTCACCATCAACACCTGCGCTACATGGCGGACATGGG00CA
 C00GGCTCCCTCAAGTTCAACATCAGAGACA0CTCACTGAGCAGCTGCTCAGTCCCTTTGTTCCAGAGGAGCAG
 CCTGGGTGCACGGTACACAGGCTGACAGGCTCATGCACTAAGGTCTGTGAAGAACGGTCTGAGACACGGGTGG
 A00CTCCTCTGAC0CTACCTGACG000CTCAGG000CAGGCTG00CTATCAAGCAGGTGTTCCATGAGCTGAGC
 CAGCAGAC00CATGGCATCAC000GCTGGG000CTACTCTCTGGACAAAGACAGCCTCTAC0CTTAAC0GTTACAA
 TGAACCTGGTCTAGATGAG0CTTCTACA0CT00CAAGCCAGCCAC0CATTCTG00CTCCTCTGTCAAG00CA
 CAACAG00CATGGGTACCACTGAAGAC0CTCAGCTCA0CTTCACCATCTCCAATCTCCAGTATTCA0CAGAT
 ATGGGCAAGGGCTCAGCTACATTCAACTCCACCGAGGGGCTCCTTCAGCAGCTGCTCAGAC00CTGTTCCAGAA
 GAGCAGCATGGG000CTCTACTTGGGTTGCCA0CTGATCTC00CTCAGG0CTGAGAAAGGATGGGGCAGCCACTG
 GTGTGGACACCA0CTGAC0CTACCA00CTGAC00CTGTGGG0000000CTGGACATACAGCAGCTTTACTGGGAG
 CTGAGTCAGCTGACCCATGGTGTCA00CA0CTGGG000CTTCTATGT00TGGACAGGATAG00CTCTCATCAATGG
 CTATGCA0000CAGATTTATCAATTCGGGGGAGTACUAGATAAATTTCCACATTTGTCAACTGGA00CTCAGTA
 ATCCAGAC0000CAGATCTCAGAGTACATCAC00CTGCTGAGGGACATCCAGGACAAGGTCA0CAGACTCTACAAA
 GGCAGTCAACTACATGACACATTC00GCTTCTG00CTGGTCA0CA0CTTGACGATGGACTC00CTGTTGGTCACTGT
 CAAGGCAATTTCTCCTCCAAATTTGGAC000CAG00CTGGTGGAGCAAGTCTTTCTAGATAAGAC00CTGAATG0CT
 CATTC0ATTGGCTGGGCTCCACCTAC0AGTTGGTGGACATCCATGTGACAGAAATGGAGTCATCAGTTTATCAA
 CCAACAGCAGCTCCAGCAGCCAGCACTTCTACCCGAATTTCA0CATCA0CA0CTACCATATTC00CAGGACAA
 AGCC0CAGCCAGGCA0CAGCAATTACCAGGGAACAAAAGGAATATTGAGGATGCGCTCA0CA0CTCTTCCGAA
 ACAGCAGCATCAAGAGTTATTTTCTGACTGTCAAGTTTCAACATTCAAGTCTGTCCCAACAGG0CAGCAGCAGC
 GGGGTGGACTC00CTGTGTAACTTCTG00CACTGGCTCGGAGAGTAGACAGAGTTGCCATCTATGAGGAATTTCT
 GCGEATGACCCGGAATGGTACCCAGCTGACAGAACTTCA00CTGACAGGAGCAGTGTCTCTGTGGATGGGATATT
 CTCCCAACAGAAATGAGCCCTTA0CTGGGAATCTGACCTTCCCTTCTGGGCTGTCACTCTCATG00CTTGGCA
 GGA0CTCCTGGGACTCA0CAGATG00TGA0CTGCGGCTGTCTGCTGACCA00CGCGG00GAGGAAGGAAGGAGA
 ATACAACGTC0CAGCAACAGTGGCCAGGCTACTACCACTCACACCTAGACCTGGAGGATCTGCAATGACTGGAAC
 TTGGCGGTG00CTGGG000CTTTCCCCAGCCAGGCTCCAAAGAGCTTGGCTGGG0CAGAAATAAACCATATT
 GGTCCG

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FIGURE 52

GCCCCGGGCGAGGTGCTGATAGCACAGTTCCTGTCACAGAGGAAGGCGGAATAAACTTATTCATTCCCAGGAACT
 CTTGGGGTAGGTGTGTGTTTTTTCACATCTTAAAGSCTCACAGACCCTGGCGCTGGACAAATSTTCCATTCCCTGAA
 GGACCTCTCCAGAAATCCGSAATTGCTGAATCTTCCCTGTTGCCCTAGAAGGGCTCCAAACCACCTCTTGACAAATGG
 GAACTGGGTGGTTAAACCACTGGTTTTTCAGTTTTGTTTTCTGGTTGTTTGGTTAGGGCTGAATGTTTTCCCTCTTT
 GTGGATGCCCTTCCTGAAATATGAGAAGGCCGACAAATFACTACTACACAAGAAAAATCCTTGGGTCAACATTTGGC
 CTGTGCCCGAGCGTCTGCTCTCTGCTTGAAATTTAACAGCACGCTGATCCTGCTTCCTGTGTGTGCAATCTGC
 TGTCTTCTCTGAGGGGACCTGCTCATTTTGCAGCCGACACTGAGAAAGCAATTTGGATCACAACTCACTTC
 CACAAGCTGGTGGCTATATGATCTGCTTACATACAGCTATTTCACATCAATTGCACACCTGTTTAACTTTGACTG
 CTATAGCAGAAGCCGACAGGCCACAGATGGCTCCCTTGCCTCCATTTCTCTCCAGCTATCTCATGATGAGAAAA
 AGGGGGGTTCTTGGCTAAATCCCATCCAGTCCCGAAACAGACAGTGGAGTATGTGACATTCAACAGCGTTGCC
 GGTCTCACTGGAGTGATCATGACANTAGCCTTGCATTCTCATGGTAACTTCAGCTACTGAGTTTCATCCGGAGGAG
 TTATTTTGAATCTTCTGGTATACTCAACACCTTTTTATCTTCTATATCCTTGGCTTAGGGATTCAAGGCATTG
 GTGGAATTGTCCGGCTCAAACAGAGGAGAGCAFGAATGAGAGTCATCCTCGCAAGTGTGACAGAGTCTTTTGAG
 ATGTGGGATGATCCTGACTCCCACTGTAGGCGCCCTTAAGTTTTGAAGGGCATCCCCCTGACTCTTGGAAAGTGGAT
 CCTTGCACCGSCTCATCTTTTATATCTGTGAAGGATCCTCCGGTTTTACCGCTCCACAGCAAGGTTGTGATTA
 CCAAGGTTGTATGCAACCATCCAAAGTTTTGGAAATGACAGATGAACAAGCTGGCTTCAGCATGGAAGTGGGG
 CAGTATATCTTTGTTAATTGCCCTCAATCTCTCTGCTGGAATGGCATCCTTTTACTTTGACCTCTGCTCCAGA
 GGAAGATTTCTTCTCCATTATATCCGAGCAGCAGGGCACTGGACAGAAAAATCTCATAAGGGCTTTGAAACAC
 AATATTCAACCAATTCACAGGATTGAAGTGGATGCTCCCTTTGGCACAGCCAGTGAGGATGTTTTCCAGTATGAA
 GTGGCTGGCTGGTGGCAGCAGGATTTGGGGTCAACCCCTTTGCTTCTATCTTGAATCCATCTGGTACAAAT
 CCAGTGTGCAGACCAACCTCAAACAAAAAAGATCTATTTCTACTGGATCTGCAGGGAGACAGGTGCCCTTT
 CCTGGTTCAACAACTGTTGACTTCCCTGGAACAGGAGATGGAGGAATTAGGCAAGTGGGTTTTCTAAACTAC
 CGTCTCTTCTCCACCGGATGGGACAGCAATATTTTGGTCAATGCAGCATTAACCTTTTGACAAGGCCACTGACAT
 CGTGACAGSCTCTGAACAGAAAACTCCTTTGGGAGACCAATGTGGGACAAATGAGTTTTCTACAAATAGCTACCT
 CCCACCCCAAGTCTGTAGTGGGATTTTTCTTATGTGGCCCTCGGACTTTGGCAAGAGGCTGGCGCAATGCTGT
 CACCGATATTCAGTCTGGATCCTAGAAAGGTTCAATCTACTTCAACAAAGAAAAATTTTGGGTTATAGGAAT
 AAGGACGGTAATCTGCATTTTTGTCTCTTTGTATCTTCAGTAATTTGAGTTATAGGAATAAGGACGGTAATCTGCA
 TTTTGTCTCTTTGTATCTTCAGTAATTTTACTTGGTCTCTGCTCAGGTTTGGAGCTCACCTTAGGTAAGAATGTG
 CCTCTCAAGCCCTTGACTCCTCGGTATTTCTTTTTTGTATCTGCAATTCAGCTTCAACTTCGTTACTTTGAGCTTCAGCACTTA
 AGAATCTCTGAAGTCTTAAAGTCTGAAAGTCTTAAAGCCCATGGATCCTTTCTCAGAAAAANTAACTGTAAAT
 CTTTCTGGACAGCCATGACTGTAGCAAGGCTTGATAGCAGAGGTTTGGTGGTTGAGAGTTATACAACHAATCCC
 AGGATATTTATCAATTCAGTGTACCATCTCTGAGTTTTGGTTTTGTAATCTTTTGTCCCTCCACCCCCAC
 ASAAGATTTCTAAGTAGGGTCACTTTTTTAAATAAAATTTATTGAATTAATTAATGATTAACATAATAATAAC
 ATAAATAATAACAAATTAACGAGAACCCCATCCCCATATAACACCAACAGTGTACATGTTTACTGTCACTTT
 TGATATGGTCTTATCCAGTGTGAACAGCAATTTATTTATTTTTGCTCATCAAAAAATAAAGGATTTTTCTTCTTCA
 CTTGATGAATGAGTCTTTTGTACTTCTTTTTGGGCTCTCCATTTGGGAAAGAAAAATCTAGAAAAGTATGCTCAT
 TGTAAATTGAATTTGATTAATAATTGCAAGTCAGCTTACTGTCTATCTTGTATTATTCTGTAAAGCGATTTGG
 AAACTTGAACCTCATGTTAGGATGACTTATTTAGTCAAGAGGAGCTCTTTATCACTATTAAGGGAGTTTATTA
 ATGCTAGTTTAAAAAATAACAAATTTATAATTTTCAAGATTTTTGTGGACTCCTACCTATATCGCTAAGGAAT
 CATTCAGCTAATAACATAAGCAAAATGCCCTTCAATCTCTATCAGAAATGCTTTTTATTTCTGCAATCTACCCAAC
 CTGGGCTTACAAGGACCACTGGCTCTGGGATGTTAGTCTCACAGTGAATCCCTAGAGGAGAGAGAGCCGAG
 GGCTCTTAAGAGAGAAACCTCACACTTCATTTGTGCCAGACAATCAACTCATTTATGATTAAGAAGATGGTTG
 TACTGAATTAGCAATTAATTAATCTATTTTTTCTACCATTAAGTGACCACGAATGAACAAAGGTTTCTTTCTAAT
 AGTTTAGGAACCTCTACGGCTTGGGGATAAACTGTTTTTGGTTTTTTTTTGTCTACTGCTGAGCACAATAA
 AGGTAGGTCAATGAACCTCATGGTGGCTAATCATGTTTCAATTAATTAACAGTAAAACAATACTGATGGTTGTT
 ACATAGGGAGGGATACCACTGCTGTTGCCAATTTGTTCAACCGGATTTCACTAATTCAGCTTTAATAAGGCTT
 TGGGAAATGCAAAATGAAACCTTGAAGACATGATTTATTATAGACAATCACTGACCAATTAACACTTCATCT
 TCAATGACCTTGATTTGGAATCTTGAACCTTACAACAGGTTCTTAATGAGAAAGGCATCACTCTTGGTCTCCAT
 GTCTAAATATATTGACACACTCACTTCAAGATATGATGGCTGCCAAATCAATATCCCAGGCTTGAATATTTA
 TGGGAGTAGGCATAAATTCGTGATTATATTCATGGTAAATGAATATAATAAATCCTATGCATAGCCACATCCAA
 GTTGAACCTGGGATGAGCAGGATACACAGAAAGCTCCTCACCTGCTTTGAGCAAGTTTTCTTGCAAGGTTGTA
 ATATGAATACCTTAATCAACAAATTTCTTATAATGTTTATATGAGTAGAAAAATCCCTCAATTTCTATTGTCAC
 TCAAAAAGTTGATTATCT

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FIGURE 53

CCCTTGGGCTCCAAACCACCTCTTGACAATGGGAACCTGGGTGGTTAACCACCTGGTTTTCAGTTTTGTTCCTGG
 TTGTTTGGTTAGGGCTGAATGTTTTCCTGTTTGTGGATGCCCTTCCTGAATATGAGAAGGCCGACAAATACTAC
 TACACAAGAAAAATCCTTGGGTCACACATTGGCCCTGTGCCCGAGCGTCTGCTCTCTGCTTGAAATTTAACAGCAC
 GCTGATCCTGCTTCTGTGTGTGCGCAATCTGCTGTCCCTTCCTGAGGGGCACCTGCTCATTITGCAGCCGACAC
 FGAGAAAGCAATTGGATCACAACCTCACCTTCCACAAGCTGGTGGCCATATGATCTGCCFACATACAGCTATT
 CACATCATTGCACACCTGTTTAACTTTGACTGCTATAGCAGAAGCCGACAGGCCACAGATGGCTCCCTTGCCTC
 CATTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTTCTTGGCTAAATCCCATCCAGTCCCGAAACACGA
 CAGTGGAGTATGTACATTACACAGCATTGCTGGTCTCACTGGAGTGATCATGACAAATAGCCTTGATTTCTCATG
 GTAATTCAGCTACTGAGTTCAATCCGGAGGAGTATATTTGAGTCTTCTGGTATACTCACCACCTTTTATCTT
 CTATATCCTTGGCTTAGGGATTCAAGGCATTGGTGGAAATGTCGGGGTCAAAACAGAGGAGAGCATGARTGAGA
 GTCATCCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATGATCGTGACTCCCACTGTAGGCGCCCTAAGTTT
 GAAGGGCATCCCCCTGAGTCTTGGAACTGGATCCTTGACACGGTCAATCTTTATATCTGTGAAAGGATCCTCCG
 GTTTTACCGCTCCAGCAGAGGTTGTGATTACCAAGGTTGTTATGCACCCATCCAAAGTTTGGAAATGCAGA
 TGAACAAGCCTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAATTGCCCCCTCAATCTCTCTCCTGGAA
 TGGCATCCCTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCTATATCCGAGCAGCAGGGGACTG
 GACAGAAAAATCTCATAAGGGCTTTTGAACAACAATATTCACCAATTCOCAGSATTTGAAGTGGATGGTCCCTTTG
 GCACAGCCAGTGAGGATGTTTTCCAGTATGAAGTGGCTGTGCTGGTTCGAGCAGGAATTGGGGTCACCCCCTT
 GCTTCTATCTTGAATCCATCTGGTACAAATTCAGTGTGACAGCCACAACCTCAAAACAAAAAGATCTATTT
 CTACTGGATCTGCAGGGAGACAGGTGCCTTTTCTGCTTCACCAACCTGTTGACTTCCCTGGAACAGGAGATGG
 AGGAATTAGGCAGAGTGGGTTTTCTAAACTACCGTCTCTTCTCACCGGATGGGACAGCAATATTGTTGGTCAT
 GCAGCATTAACCTTTGACAAGGCCACTGACATCGTGACAGGTCTGAAACAGAAAACCTCCTTTGGGACACCAAT
 GTGGGACAATGAGTTTCTACAATAGCTACCTCCACCCCAAGTCTGTAGTGGGAGTTTCTTATGTGGCCCTC
 GGACTTTGGCAGAGAGCCTGCCCAATGCTGTACCGATATTCAGTCTGGATCCTAGAAAGSTTCAATTCATC
 TTCAACAAAGAAAAATTTTGAAGTTATAGGAATAAGGACGGTAATCTGCATTTGTCTCTTTGTATCTTCAGTAA
 TTTACTTGGTCTCGTCAGGTTTGAAGCAGTCACTTTAGGAAG

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FIGURE 54

GGGCTCCAAACCACCTCTTGACAAATGGGGAAACTGGGTGGTTAACCACTGGTTTTTCAGTTTTGTTTCTGCTTGT
TGGTTAGGGCTGAATGTTTTCCCTGTTTGTGGATGCCTTCCTGAAATATGAGAAGGCCGACAAATACTACTACAC
AAGAAAAATCCTTGGGTCTTGGAACTGGATCCTTGCACCGGTCATTCTTTATATCTGTGAAAGGATCCTCCGGT
TTTACCGCTCCCAGCAGAAGGTTGTGATTACCAAGGTTGTTATGCACCCATCCAAAGTTTTGGAATTGCAGATG
AACAAAGCGTGGCTTCAGCATGGAAAGTGGGGCAGTATATCTTTGTTAATTGCCCCCAATCTCTCTCCTGGAATG
GCATCCTTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTTCATATCCGAGCAGCAGGGGACTGGA
CAGAAAATCTCATAAGGGCTTTCGAACAACAATATTCACCAATTCCCAGGATTGAAGTGGATGCTCCCTTTGGC
ACAGCCAGTGAGGATGTTTTCCAGTATGAAGTGGCTGTGCTGGTTGGAGCAGGAATTGGGGTCACCCCTTTGC
TTCTATCTTGAAATCCATCTGGTACAAATTCCAGTGTGCAGACCACAACTCAAAACAAAAAGGTTGCTCATG
CAGCATTAAACCTTTGACAAAGGCCACTGACATCGTGACAGGCTCGAAACAGAAAACCTCCTTTGGGAGACCAATG
TGGGACAATGAGTTTTCTACAATAGCTACCTCCCACCCCAAGTCTGTAGTGGGAGTTTTCTTATGTGGCCCTCG
GACTTTGGCAAGAGCCCTGCCAAATGCTGTACCGATATTCAGTCTGGATCCTAGAAAGGTTCAATTCTACT
TCAACAAAGAAAATTTTGGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAGTAAT
TTACTTGGTCTCGTCAGGTTTGAGCAGTCACTTTAGGA

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FIGURE 55

GGGCTCCAAACCACCTCTTGACAATGGGAACTGGGTGGTTAACCCTGGTTTTTCAGTTTTGTTTCTGGTTGTT
TGSTTAGGGCTGAATGTTTTCTGTTTTGTGGATGCCCTTCCTGAAATATGAGAAGGCCGACAAATACTACTACBC
AAGAAAAATCCTTGGGTCAACATTGGCCCTGTGCCCCGAGCGTCTGCTCTCTGCTTGAATTTTAAACAGCAGCGTGA
TCCTGCTTCCTGTGTGTGCAATCTGCTGTCTTCTGAGGGGGCACCTGCTCATTTTGCAGGCCGACACTGAGA
AAGCAATTGGATCACAACCTCACCTTCCACAAGCTGGTGGCTATATGATCTGCCTACATACAGCTATTCACAT
CATTGCACACCTGTTTAACTTTGACTGCTATAGCAGAAGCCGACAGGCCACAGATGGCTCCCTTGCCTCCATT
TCTCCAGCCTATCTCATGATGAGAAAAAGGGGGGTTCTTGGCTAAATCCCATCCAGTCCCGAAACACGACAGTG
GAGTATGTGACATTCACCAGCATTGCTGCTCTCACTGGAGTGATCATGACAATAGCCCTTGATTCTCATGGTAAC
TTGAGCTACTGAGTTCAATCCGGAGGAGTTATTTTGAAGTCTTCTGCTATCTCACCACCTTTTATCTCTCATA
TCCTTGGCTTAGGGATTACGGCCTTGGTGGAAATTGTCCGGGTCAAACAGAGGAGAGCATGAATGAGAGTCAT
CCTCGCAAGTGTGCAGACTCTTTTGAGATGTGGGATGATCGTGACTCCCACCTGTAGGCCGCCCTAAGTTTGAAGG
GCATCCCCCTGAGTCTTGGAGTGGATCCTTGCACCGGTCAATCTTTATATCTGTGAAAGGATCCTCCGGTTTT
ACCGCTCCCAGCAGAGGTTGTGATTACCAAGTTGTATGACCCCATCCAAAGTTTTTGAATTGCAGATGAAC
AAGCGTGGCTTCAGCATGCAAGTGGGGCAGTATATCTTGTTAATTGCCCCCAATCTCTCTCTTGGAAATGGCA
TCCTTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCTATCCGAGCAGCAGGGGACTGGACAG
AAAATCTCATAAGGGCTTCCGAACAACAATATTCACCAATTCCCAGGATTGAAGTGGATGGTCCCTTTGGCACA
GCCAGTGAGGATGTFTTCCAGTATGAAGTGGCTGTGCTGGTTGGAGCAGCAATTGGGGTCACCCCCCTTTGCTTC
TATCTTGAAATCCATCTGGTACAAATTCAGTGTGCAGACCACAACCTCAAACAAAAAASGTTGCTCATGCAG
CATTAACCTTTGACAAGGCCACTGACATCGTGACAGGTCTGAAACAGAAACCTCCTTTGGGAGACCAATGTGG
GACBATGAGTTTTCTACAATAGCTACCTCCCACCCCAAGTCTGTAGTGGGATTTTCTTATGIGGCCCTCGGAC
TTTGGCAAGAGCCTCGGCAATGCTGTACCGATATTCAGTCTGGATCCTAGAAAGGTTCAATTCTACTTCA
ACAAAGAAAATTTTGAAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAGTAATTTA
CTTGGTCTCGTCAGGTTTGAGCAGTCACCTTAGGAAG

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FIGURE 56

GGACTGCTTTGTAACGCTAAGATTGCAGACAGAAATAGCACACAACCCTGTGAGCTGTATGCGATTTCAGAAA
CCAAGACCAAAATTTTGCTCACTTTCAATTAATCAGTTGCTCAGATAGAAGGAAATGACATCTGGTTCTGTCTTCT
TCTACATCTTAATTTTGGAAAATATTTTCTCATGGGGGTGGACAGGATGTCAAGTGTCCCTTGGCTATTTT
CCCTGTGGGAAACATCACAAAGTGCTTGCCCTCAGCTCCTGCCTGTAAAGGTGTGGACGACTGGGGGANTCAGGC
CGATGAGGACAACTGTGGAGACAAATGGATGGTCCATGCCAATTTGACAAATATTTTSCCASTTACTACAAAA
TGACTTCCCAATATCCTTTTGAGGCAGAAACACCTGAATGTTTGGTGGGTTCTGTGCCAGTGCAATGTCTTTGC
CAAGGTCTGGAGCTTGACTGTGATGAAACCAATTTACGAGCTGTTCATCGGTTTCTTCBAATGTGACTGCAAT
GTCACFTCAGTGGAACTTAATAAGAAAGCTTCCTCCTGATTGCTTCAAGAATTATCATGATCTTCAGAACCTGT
AAGTGCAGAAACAAATAAGATTACATCCATCTCCATCTATGCTTTCAGAGGACTGAATAGCCTTACTAACTGTAT
CTCAGTCATAACAGAATAACCTTCCTGAAGCCGGGTGTTTTTGAAGATCTTCACAGACTAGAATGGCTGATAAT
TGAAGATAATCACCCTCAGTCGAATTTCCCCACCAACATTTTATGGACTAAATCTCTTATTCTCTTAGTCCTGA
TGAATAACGTCCCTCACCCGTTTACCTGATAAACCTCTCTGTCAACACATGCCAAGACTACATTGGCTGGACCTT
GAAGGCAACCAATATCCATAATTTAAGAAATTTGACTTTTATTTTCTGCAGTAATTTAACTGTTTTAGTGATGAG
GAAAAACAAAATTAATCACTTAAATGAAAATACTTTTGCACCTCTCCAGAACTGGATGAATGGATTTAGGAA
GTAATAAGATTGAAAATCTTCCACCGCTTATATTTCAAGGACCTGAAGGAGCTGTACAAATTTGAATCTTTCCTAT
AATCCAATCCAGAAAATTCAGCAAAACCAATTTGATTATCTTGTCAAACCTCAAGTCTCTCAGCCTAGAGGGAT
TGAAATTTCAAATATCCAACAAAGGATGTTTAGAAGCTCTTATGAATCTCTCTCACATATATTTTAAAGAAATCC
AGTACTGTGGGTATGCAACACATGTTCCGACGCTGTAAACCAACACCTGATGGAATTTTCACTCTCTAGAGAACTCTC
TTGGCAAGCAATTTTTCAGAGAGTATTTGTCTGGGTTGTATCTGCAGTTACCTGCTTTGGAAACATTTTGTGCAAT
TTGCATGCGACCTTATATCAGGTCTGAGAACAAAGCTGTATGCCATGTCAATCAATTTCTCTGCTGTGCCGACT
GCTTAATGGGAATATATTTATTCGTGATCGGAGGCTTTGACCTAAAGTTTCTGAGGAGATACAATAAGCATGCC
CAGCTGTGGATGGAGAGTACTCATTGTCAGCTTGTAGGATCTTTGGCCATTTCTGTCCACAGAAATATCAGTTTT
ACTGTTAACATTTCTGACATTTGGAAAAATACATCTGCATTGTCTATCCTTTTATGATGTCTGAGACCTGGAAAAF
GCAGAACAAATACAGTTCTGATTCTCAATTTGGATTACTGGTTTTATAGTGGCTTTCATTCCATTGAGCAATAG
GAATTTTTCAAACACTACTATGGCACCATGGAGTATGCTTCCCTCTTCATTGAGAAGATACAGAAAGTATTGG
AGCCAGATTTAATTCAGTGGCAATTTTTCTTGGTATTAATTTGGCCGCTTTTATCATCATAGTTTTTTCCTATG
GAAGCATGTTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAGAGATG
ATCCTTGCCAAACGTTTTTTCTTTATAGTATTTACTGATGCATTATGCTGGATACCCATTTTGTAGTGAATTT
TCTTTCACTGCTTCAGGTAGAAATGCCAGGTACCAATACCTCTTGGGTAGTGATTTTATTTCTGCCCATTAACA
GTGCTTTGAACCAATTTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTATCGGTTTTGGTATAAC
TACAGACAAAGAAAATCTATGGACAGCAAAGGTGAGAAACATATGCTCCATCATTCATCTGGGTGGAAATGTG
GCCACTGCAGGAGATGCCACCTGAGTTAATGAAGCCGGAACCTTTTACATACCCCTGTGAAATGTCACTGATTT
CTCAATCAACGAGACTCAATTCCTATTCTGA

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FIGURE 57

TAGAGATCCCTCGACCTCGACCCACGCGTCCGAGGAAAGAAAAAGAGGAATGGAAGACAGACAGAGAAAGGAA
 ATGGGAGTGGAAAGGAGGGAGGAGTGTCTTTGTAAGATTGCGACAGAAATAGCACACAACCACTGTGA
 GCTGTATGCGATTCCAGAAACCAAGACCAATTTTGTCTCACTTTTATTAAATCASTTGCTCAGATAGAAGGAAATG
 ACATCTGGTCTCTCTCTCTCTACATCTTAATTTTGGAAAAATATTTTCTCATGGGGCTGGACAGGATGTCAA
 GTGCTCCCTTGGCTATTTCCCTCTGTGGGAACATCACAAAAGTGTCTGCTCAGCTCCTGCACTGTAACGGTGTGG
 ACGACTGCGGGAATCAGGCCGATCAGGACCACTGTGGAGACAACAATGGATGGTCTCTGCAATTTGACAAATAT
 TTTGCCAGTTACTACAAAATGACTTCCCAATATCCTTTTGAGGCGAGAAACACCTGAAATGTTTGGTGGGTTCTGT
 GCCAGTGCAATGTCTTTGCCAAGGTCTGGAGCTTGACTGTGATGAAACCAATTTACGAGCTGTTCCATCGGTTT
 CTTCAAATGTGACGCAATGTCACTTCAGTGGAACTTAATAAGAAAGCTTCTCTCTGATTCGTTCAAGAATTAT
 CATGATCTTCGAAAGCTGTACCTGCAAAACATAAGATTAACATCCATCTCCATCTATGCTTTCAGAGGACTGAA
 TAGCCTTACTAACTGTATCTCAGTCATAACAGAAATACCTTCCGAAAGCCGGGTGTTTTTGAAGATCTTCACA
 GACTAGAATGGCTGATAATTGAAGATAATCACCTCAGTGGAAATTTCCCCACCAACATTTTATGGACTAAATCT
 CTTATTCTCTTAGTCTGATGAATAACCTCTCACCCCTTACCTGATAAACCTCTCTGTCAACACATGCCAAG
 ACTACATTTGGCTGGACCTTGAAGGCCAACCATATCCATAATTTAAGAAATTTGACTTTTATTTCTTGCAGTAATT
 TAACTGTTTTAGTGATGAGGAAAAACAAATTAATCACTTAAATGAAAATACTTTTGCACCTCTCCAGAACTG
 GATGAATTTGATTTAGGAAGTAATAAGATTGAAATCTTCCACCGCTTATATTCAAGGACCTGAAGGAGCTGTC
 ACAATTGAATCTTTCTTATATCCAAATCCAGAAATTTCAAGCAAAACCAATTTGATTTATCTTGTCAAACCTCAAGT
 CTCTCAGCCTAGAAGGGATTTGAAATTTCAATATCCAAACAAAGGATGTTTAGACCTCTTATGAATCTCTCTCAC
 ATATATTTTTAAGAAATTCACSTACTGTGGGTATGCGACCATATGTTGCGAGCTGTAAACCAACACTGATGGAAT
 TTCATCTCTAGAGAATCTCTTGGCAAGCATTTATTCAGAGAGTATTTGTCTGGGTGTATCTGCASTTACCTGCT
 TTGGAAACATTTTTGTCTCTTGCATGCGACCTTATATCAGGCTCTGAGAACAAGCTGTATGCCATGTCAATCATT
 TCTCTCTGCTGTGCGACTGCTTAATGGGAATATATTTATCTGATCGGAGGCTTTGACCTAAAGTTTCTGTG
 AGAATACAAATAGCATGCCAGCTGTGGATGGAGAGTACTCATTGTGAGCTTGTAGGATCTTTGGCCNTTCTGT
 CCACAGAAGTATCAGTTTACTGTTAACATTTCTGACATTTGGAAAAATACATCTGCATTGTCTATCCTTTTAGA
 TGTGTGAGACCTGGAAATGCAGAACATTAAGTTCGATTTCTCATTGGATTACGTTTTATAGTGGCTTT
 CATTCCATTGAGCAATAAGGAATTTTCAAAAACACTACTATGCCACCAATGGAGTATGCTTCCCTCTTCATTGAG
 AAGATACAGAAAGTATTGGAGCCGAGATTTATTCAGTGGCAATTTTCTTGGTATTAATTTGGCCGCAATTTATC
 ATCATAGTTTTTCTTATGGAAGCATGTTTTATAGTGTCTCATCAAAGTGCCATAACAGCAACTGAANTACGGAA
 TCAAGTTAAAAAAGAGATGATCCTTGCCAAACGTTTTTCTTTATAGTATTTACTGATGCATTATGCTGGATAC
 CCATTTTTGTAGTGAATTTCTTTCACTGCTTCAGGTAGAAATACCAGGTACCATAACCTCTTGGGTAGTGATT
 TTTATTTCTGCCCATTAACAGTGTCTTGAACCAATTTCTCTATCTCTGACCAACAAGACCAATTAAGAAATGAT
 TCATCGGTTTTTGGTATAACTACAGACAAAGAAAATCTATGGACAGCAAAAGGTGAGAAACATATGCTCCATCAT
 TCATCTGGGTGGAAATGTGGCCACTGCGAGAGATGCCACCTGAGTTAATGAGGCGGACCTTTTACATACCCC
 TGTGAATSTCACTGATTTCTCAATCAACGAGACTCAATTCCTATTCACTGACTCTGAAATTCATTTCTTC
 GCAGAGAATACTGTGGGGGTGCTTCATGAGGGATTTACTGGTATGAAATGAATACCACAAAATTAATTTTATAAT
 AATAGCTAAGTAAATATTTTACAGGACATGAGGAAAAATAAAAATCACTAATGCTCTTACAAAGGGAGTAA
 TTATATCAATATGTATATATATATAGTAGACATTTTGCATAAGAAATTAAGAGAAATCTACTTCAGTAACATTTC
 ATTCATTTTTCTACATGCAATTTATGASTACCCACTACTATGTGCATAGCATTGCAATATAGTCTTGGAGTA
 GACAGTGCAGAACCTTTCAATCTGTAGATGGTGTAAATGACAAAAGACTATACAAAGTCCATCTGCASTTCTT
 AGTTTAAAGTAGAGCTTTACCTGTGATGTGCATCAGCAAGAAATCATAGGCACCTTTTAAATGAAGCTTTAAGT
 TTGGAAT

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FIGURE 58

GATCCATTGTGCTGGCGCGGATTCTTTATCACTGGAAGGAGGAGGAGGGGGAGAGTCGCTCCCGCCSGGCGAGC
ATGGGGGCCCTGGCTCGAGGCCCTGCTGCTGGCGCTCCTGTGCTTGGCTCTTTGCGAGGGGCTGTGGTGAG
 AGTCCCCACAGCGACCCCTGGTTGAGTGGTGGGCACTEAGCTGGTCATCCCCCTGCAACGTCACTGACTATGATG
 GCCCCAGCGAGCAAACTTTGACTGGAGCTTCTCATCTTTGGGGAGCAGCTTTGTGGAGCTTGCAGCACCTGG
 GAGGTGGGGTTCCAGGCCAGCTGTACCAAGAGCGGCTGCAGAGCGGGCAGATCCTGTTAAGGCGGACTGCCAA
 CGACGCCCTGGAGCTCCACATAAAGAACGTCACGCCCTTCAGACCAAGGCCACTACAAATGTTCAACCCCCAGCA
 CAGATSCCACTGTCCAGGGAACTATGAGGACACAGTGCAGGTTAAAGTGGCTGGCCGACTCCCTGCACGTGGGC
 CCCAGCGCGCGGGCCCCCGCGAGCCTGAGCCTGCGGGAGGGGAGCCCTTCGAGCTGGCTGCACGCCCGCTC
 CGCCTCGCCGCTGCACACGCACTTCCGCTGCTGTGGGAGGTGCACCGCGGCCCGGCCAGGCGGAGCTCCTCG
 CCTGACCCACGAGGGCAGGTTCCACCCGGGCTGGGTFACGAGCAGCGCTACCAAGTGGGAGCTGCGCCTC
 GACACCGTGGGCGAGCGACGCTTACCGCTCTCAGTGTCCCGGCTCTGTCTGCCGACCAGGGCTCCTACAGGTG
 TATGCTCAGCGAGTGGATCCCGGAGCAGGGCAACTGGCAGGAAATCCAGAAAGGCCGTGGAACTGCCACCG
 TGTGATCCAGCGEACAGTCTGTGCGAGCAGCTGTGCCCAAGAAATGTGTCTGTGGCTGAAGGAAGGAACTGGAC
 CTGACCTGTACATCACACAGACCGAGCCGATGACGTCCGGCCCGAGGTGACGTGGTCTTCAGCAGGATGCC
 TGACAGCACCCCTACCTGGCTCCCGCTTGTGGCGCGGCTTGACCGTGATTCCCTGGTGCACAGCTCGCCCTCATG
 TTGCTTTGAGTCTGTGGATGCAGCTCCTACCATTTACTGCTTGGGATGTTAGCAAAGAAACTCTGGCTAC
 TATTACTGCCACGTGTCCCTGTGGGCACCCGGACACCAACAGGAGCTGGCACAAAGTGGCAGAGGCTGTCTTC
 CCGAGCTGCTGTGGGTGTGACCTGGCTAGAACCAAGCTTCCAGGTGTACCTGAATGCTTCCAGGTCCCCGGGT
 TTGGGATGACCCACAGAGCTGGCATGCCGGGTGGTGGACCGAAGAGTGGGGAGGCGAATGTCCGATTACG
 GTTTCCTGGTACTACAGGATGAACCGCGCGCAGGACAAATGTGGTGACCGAGCTGCTTGCAGTCACTGGACGG
 GSACTGGACGCTAAAATATGGAGAGAGGAGCAAGCAGCGGGCCAGGATGGAGACTTTATTTTTTCTAAGGAAC
 ATACAGACAGCTTCAATTTCCGATCCAAAGGACTACAGAGGAAGACAGAGGCAATTATTTACTGTGTTGTCT
 GCCTGGACCAACAGCGGAACAACAGCTGGGTGAAAGCAAGGATGTCTTCTCCAAGCCTGTAAACATATTTTG
 GGCATTAGAAGATTCCGTGCTGTGCTGAAAGGAGGCGAGCCAAAGCCTTTCTTTGCTGCCGGAATACATTTG
 AGATGACTTGCAAAGTATCTTCCAAGAAATTTAAGTCGCCACGCTACTCTGTTCTCATCATGGCTGAGAAGCCT
 GTCCGCGACCTCTCCAGTCCCAATGAAACGAAGTACNTCATCTCTCTGACCAGGATTTCTGTGCTGAAGCTGGA
 GAATGGACAGATGCATCAGCGTGCATGGCGTTGTTTACAAAAAGTGCAGGAGGATGAGTTCCGCTATCGAA
 TGTACCAGACTCAGGTCFCAGACGCGAGGGCTGTACCGCTGCATGTTGACAGCCTGGTCTCCTGTCAAGGGCAGC
 CTTTGGCGAGAAGCAGCAACCACTCTCTCCAATCCTATTGAGATAGACTTCCAACCTCAGGTCCTATATTTAA
 TGCTTCTGTGCATTCAGACACACCATCAGTAATTCGGGAGATCTGATCAAAATGTTCTGTATCATCACTGTG
 AGGGAGCAGCACTGGATCCAGATGACATGGCCTTTGATGTGTCTGCTGCTTTGCGGTGCACCTTTTGGCCTGGAC
 AAGGCTCCTGTGCTCCTGTCTTCCCTGGATCGGAAGGCGATCGTGACCACTCCCGGAGGGAGCTGGAAGAGCGA
 CCTCAGCCTGGAGCGCGTGAATGTGCTGGAATCTTGGCTGCAAGTGCATGGCTCCGAGGACAGGACTTTGGCA
 ACTACTACTGTTCCGTGACTCCATGGGTGAAGTCACCAACAGGTTCTTGGCAGAAGGAGGCAGAGATCCACTCC
 AAGCCCGTTTTTATRACTGTGAAGATGGATGTGCTGAAGCGCTTCAAGTATCCCTTGTGATCGGCATCGGTCT
 GTCCACGGTCATCGGCTCCTGTCTGTCTCATCGGCTACTGCAGCTCCCACTGGTGTGTAAGAGGAGGTTTC
 AGGAGACACGCGCGAGCGCGCAGGCTCATGTGATGGAGATGGACTTAGGCTGGCCCGCGAGGGGAGTGACAG
 AGGGACGTTCTAGGAGCAATTTGGGGCAAGAGAGGACAGTGATATTTTAAACAAAGTGTGTTACACTAAAAAC
 CAGTCCCTCTCTAATCTCAGGTGGGACTTTGGCGCTCTCTCTTTTCTGCATGTCAAGTCTCGAGCGCGGACATGTT
 TACCGCACACGCGCTCTTCTTCCACGGCACTTTCTGATGTAACAATCGAGTGTGTGTTTTCCCAACTGCCAGT
 GATAAAGAACTCCGCGCCAGCACAAATGGATCTCGAGGGATCTTCCATACCTACAGTTCTGCGCCTGCAGGTC

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FIGURE 59

CCCACGCGTCCGCGTAAATCACTTCTTGGAGGTGCCGTGCACGCCGGTCTCTGGGAGCAGCGCGGCTCCCGGGG
 GTGCGGGAGCCCCACTCCTCCGTGGTGTGTTCATTTGCTTCCCACATCTGGAGGAGCTGACGTGCCAGCCTCC
 CCCAGCACCCACCCAGGACGCGGAGGCAATGAGCCGCTCAAGGCACCTGGGCAAAATCCGGAAGCGTCTGGAAGAT
 GTCAAGAGCCAGTGGGTCCGCCCCAGCCAGGGCTGACTTTAGTGACAACGAGAGTGCCCGGCTGGCCACGGACGC
 CCTCTTGGATGGGGTTCTGAAGCCTACTGGCGGGTGCTCAGCCAGGAAGGCGAGGTGGACTTCTTGTCTCTGG
 TGGAGGCCCCAGTACATCCAGGCCCCAGGCCAGGGAGCCCCGTGTCCCCCAGACACCTGGGAGGGGGCGGAAGCA
 GGGCCCTAAGGGACTGGACTCCAGCTCCCTACAGTCCCGCACCTACTTCCCTGTGGGCTCAGAGGGCAGCGAGCC
 GGGCCCTACTGCACAGCTGGGCTCAGCTGAGAAGCCCTACCTGAAGGAAAAATCCAGCGCCACTGTGTACTTCC
 AGACCGTCAAGCACAAACAACATCAGAGACCTCGTCCGCGCTGCATCACCCGGACTAGCCAGGTCTGTGTCTATC
 CTGATGGATGTGTTCAGGATGTGGAGATCTTCTGTGACATTTCTAGAGGCAGCCAAACAAGCGTGGGGTGTTCGT
 TTGTGTGCTCTTGGACCGGGAGGTGTGAAGCTCTTCCAGGAGATGTGTGACAAAGTCCAGATCTCTGACAGTC
 ACCTCAAGAACATTTCCATCCGAGTGTGGAAGGAGAGATATACTGTGCCAAGTCAGGCAGGAAATTCGCTGGC
 CAAATCCGGGAGAAGTTCTATCATCTCGGACTGGAGATTTGTCTGTCTGGATCTTACAGCTTCACCTGGCTCTG
 CGGACAGGTGCACCGGAACATCCTCTCAAGTTCCAGGCCAGGCGGTGGAGCTGTTTGACGAGGAGTTCCGCC
 ACCTCTACGCTCTCTCCAGGCTGTATGGGCTGAAGTCCCCCGGGCTGGTGGCCCCCGTCCCCCCCCGAGCA
 GGGGGGGCAATGGCCGCTTAGCAGCAGCAGTGGCTTCCCGCAGTGACCGCACGTCTCTCCAGCCCTTCAGCGG
 CCGCTCGGCAGGCAGCCACCCCGGTACCCGAAGTGTGTCCGCTCTTCAGGGCCCTGTAGCCCGCGGCCCCCAG
 ACCCGCTCCACGCCCCCGGTTCCAGCCCCACCAAGGCTTTGGGGAGCCCGAGTCCCCAGGCCCCACTCTCC
 CCGCGGCCCCCAGCAGGCCCCCGCCCGCTGTCTACAGCAACCTGGGGGCTTACAGGCCACCGGGCTGACGCT
 GGAAGAGCTGGGCTGTGTGCGGAGGCTGACTCCAACTGGAGGGCCCTTCTGCAGGCTTCCCTCACTTCTGA
 GGTCCCATCCCCCTGCTGCCCTCCGACGGCCAGGGTGGGCACTCCCTGAGACCCAAAGACCCACCTCAACGAC
 GAGTGGCTTGAAGCACTTCCCTTTGAARAGACATCBAATCACTGCCATGGTTCATGTTCACAGGCCCCAG
 GCCATCCACTTGCCGCCCCCACCAGTTCTTGGGTCCCCGCTCTAGTTTGACCTGTGCAGCACATTCBGAAG
 GTTCCAGGGGAGGTGTGTGGGCAGCTAGAGGACAAATCATGAAACAGAGTCCCTGTCTTCCAGAGATCATCC
 GGGGCTTTAAATATTAATGGCCCCCAAACTCCGTAAGAACAGGAAATGCAGCCCAAGTTTACAAATGGGTAA
 ACAGAGGCACTGAGAGATAGATGGTAGTTTGGTACTTCTGGTTCAGGTGCCAGGAATGGTCCACTCCCAAGA
 AATTCAGGAAGAAAGACTGAGGAGAAGGTGTGGGACATTTCTGGATGTTTGGGAGAGTTGGGGAAACTCCTC
 CTCTTAGGAAGGCTAATACTAGGGTATCTTGGGCCCAATGAATTAGGGGTGAGGCCCCAGAACCCGTTATCT
 ATGAGTTGTATGGGGAGCCATCTGAAGCTGTAGCCACCAGGGATGCAGCTAGCTGAGGAGTTTGGGGTGTGG
 GTTGGACAAGGCAGGTTAGTAGACTCAGATTCTTGTCTCAAGAGGCTTGGGCTGGCTGGAGGTCCCTGGAGT
 CTAGACTGGACCTAGGAGCTTGAGTTGTCAAGGGCCAGCACTGGCCCCACTGCAGTGCCACAGGCCAGTCTTGAG
 CAGCAGGGAGGGCTCAGCTGTCCCCAGTCCGGTGGCTGTGACCAGGCTGGTCACTCTGAGGAATTAATGC
 TGAACCTCACAAGCCCCATCATTCATTTCTTCTCAATTCACAGTGCCCTCTPTTGTCTGGGGTGAAGTAGG
 TCCTGAGGGCAGCAGCTAGCTGAGTGCAAGAAATATAGGATGCTTAGAAAGCATACAGGAGGGGCCAGGCTG
 GTGGCTCATGCTGTAAATCCAGAACTTTGGGATGCCAAGGTGGTTGGATTACCTGAGATCAGGTGGATTACCT
 GGTCTCGAGACAGGCTGACCAATATGGTGAACCCCGTCTCTACTAAAAATACAAAATTAGGCTGAGACAGG
 AGAATTCUTTGAACCCAGGAAGCAGAGGTTGCAATGAGCTGAGATTGCATCACTGCACTCCAGCATGGGCAACA
 AAGCAAGACTCCGTACAGAAAAAATAAATAA

[illegible]

GAAGACACACACACTTCTATGTAATGCTACCTGCAAGTCTCCCTAGAAAAGCAGTTTCTGAGGTTGAAACCAAT
GAAGCCAGGTAAATATTGCAAGGAGGCTGTAATTTTAGCAGACCTACCAACAACACATGATGTAGGAAGCTCATT
TTTTAATTTCTGGAGCCTTTTAATTTTTCTTTAGAAAAGTGTATAAATAATTGCAAGTGTCTGCTTTGCTTCCAAA
ACTGGGCGAGTGAATTAACAACAACAGACAACAACAGCGCGAGCTCATCTGGGCGGTCAATGGAGTTTCTTGAAG
AACGTATCTTGTGAATGTAAGCTGCCAAGATGTAATGCTTTCCACATAGAAAAGGAGCTGCCAAATGAACAC
TTCATAGCAATGTGGAATCCCAACAGAAACGGTGAATTAAGATCAGTGTCCGAGAGAGACAGACAGAGAGCTG
GAGTCAGGAGGCAATGCTACCACCTGCCACAGTGGCTCCAAGCCACAGAAAAGGGGGGCAATGAGTACGCTTATGC
CAAGTGGAAACTCTGTTCTGCTTCAGCAATATGCTTCATTTTCATGATTGCAGAGGTGCTGGGTGGGCACATTG
CTGGGAGTCTTGTCTGTTGTACAGATGCTGCCACCTCTTAATGTGACCTGACCAAGTTTCTGCTCAGTCTCTTC
TCCCTGTGCTTGTCTCATCGAAGCTTCCCTCTAAGCGGCTGCATTTGGATGGCAGCGAGCAGAGATCTTGGTGC
CCTGCTCTCCATCTCTGTCATCTGGCTGGTGTGCTGGCGTGCCTGAGTGTACCTGGCATTGAGCCCTGCTGTATC
CTGATTTACAGATCCAGGCGACTGTGATGATCATCGTTTCCAGCTGGCAGTGGCGGGCCAACTTTGACTAATC
GTGTTTGTGCAACAGAGATGCTTGGGCCAATCACAAGGAAGTACAAGCCATGCCAGCGTCAGAGCTGCTTT
TGTGCATGCCCTTGGAGATCTATTTAGAGTATCAGTGTGCTAAATGAGTGCATTTATATCTACCTTTAAGCCAG
AGTATAAATAGCCGACCCAACTGCAATTCATCTTTTCCATCTGGTCTTGGCCAGCAGCAGTCACTATCTTA
AAGGACTCTCTCATCTTACTCATGGAAGGTGTGCCAAGAGAGCTGAAATACAGTGGTGTGAAGAGCTTATTT
AGCAGTCGACGGGGTGTCTGTCTGTGCAACAGCTGCACCTGTGGTCTCTAACATGAATCAGTAATCTCTCAG
CTCATGTTGCTACAGCAGCCAGCGGGACGCCAAGTGTGTCGAGAGAAATGCTAAAGCCCTTAGCAAAAGC
TTTACAGTGCATCTCACTCACCATTGATGGAATCTCCAGTTGACCCAGCAGCCCGACTGCTTTCTGTGAAGA
CCCTGTGACTAGCTCAGTCAACCGTCACTTTCCCAATTTGACAGCGCCACCTTCAACATGCTGCTATGAG
TTTCTGCATCATAGAAAATAAGGACCCAAAGGAAGAAATTCATGTCATGCTGCAATGCACATTTATCTATTTA
TTTAGTTCCTAATCAACATGAAGGAGAGGCACTGAGATCCATCAATCAATTTGATATATATCATGATCAGTACCT
GTGTTCAATTCAGGAAATGTGATATAGATTAATCTGATGAGTGGAGCGGAAGTAAACAGCTGTTTGAATCTCGG
CAATAGCAAAATCATCTCTCTTCCATTAATGCTCTTGAGAACAATGAGTAAATTTGAATCTGAGAAAGTCTT
ACTAGCAAAATCACTGGAAGGGACAAATAGTCAAAAATTTTACCAAAACATTAGAAAACAAAATTAAGGAGAGCC
AAGTCAGGAATTAAGTGTCTGTATGCTAAAGCCACATTAGAACTTGGTCTCTCAACAGCGTGAATGTGA
TTTTTTTTTCTACTCTGAATGGAATATGATGAATATACAGAGAGTGTCTTACAACTAATTTTATTTACTT
GTCAATTTTGGCAATTAATCCCTCTTATTTCTAATTTCTAATTTGTTTATTTCAAACCTTTATATATCACTG
TTCAAAAGGAATTAATTTCACTTACAGAGTGTCTTAAACACTGGCCAGCCAGCAAGAAATGTGGTTATGAGAGCC
CAGAGAGCTTCAAGAAACCCGACAAAACATTCGAGTTGACCCACCAAGTTTGTGCCACAGATATTTAGAT
ATTTACCTGCAAGAGGAATTAAGCAGATGCAACCAATTCATTGAGTCCAGCAGCAGATGATGTGAGCAGTGTCTT
GTGCTAGACATTTGGGCTTAGCATTGAACTATAAAGAGGAATCAGACGAGCAAGTGTCTGTGCTGTGCTGAG
CAACTCAACACTATCTGTGAGAGTAACTGAAGATGTGAGGCGCAACCTCTGGAATTCCTATGTCACTGGCT
TTGGTTTGGAAACCTGGAGTCTCTGCAATTTTAAATTTTACCCAGAGATGCTCTTAAGATGAGCCATAGTCTAG
AAGATGTGCAACCAAGAGGATTCATTGAGTGGGACAGCTAGACATACATTTGGCAGCTACAATAGTATCATGA
ATTGCAATTCAGTCTAGTGGGTATAAAGGAAACGATGGATATTTGCCGGATGGGCATGGCCAGTGTGTTTAC
GTCATTGAGTGTGAGCTCTGCTGGACTTTGAATTACATATGGAGGCTCTCCAGGAGACGAGAAGAGAAAGGA
CAATCTAGGCAAAAAGAGACTAGGCACAGGCACACTTATGTTTGTCTGTGAGCTTTTATGTTGAAAAGCAGAA
ATACATGATGCAAGAAACCTCTCCACGCTGTGATTTTTTAAACTACATCTTTTGAACCTTTATGTTTATGA
GTATTGTAGAGAACAGCAGATAGGCTTAGATGATTTTTATGTTTGTGTCAGACTCTAGCAAGGTATCAGAAAC
CTAGCAGGCAATTAATATTTGAGGCAATGACTGTGAGCTATATCTGGGCTGTCTATTTATTTATCTATAT
TTTTGATTTTTTTTGAATTTGAGGCGGACGAAAACATTTGACTTTGACTGAGGAGGTCAATCTGTGCTGCT
TCTGCAATCAATCAGCAGCACTGAATTAACACTACTTAGCATTTCTGCTGAGCTTTCCCTGCTCAGTAGAGACAAA
TATACTCATCCCCACCTCAGTGAAGTGTGTTAGGCAACCAAGGATTAAGAGTGTGCTGAGTTTCCCAACGCTCTCT
GCCACATCGGGTCTCAAAATGGAAGAAATGTTTATGCCAAATCACTTTTCTGCTCTGAAGGACCACTGAATG
GTTTTGTTTTTCCATATTTTGCATAGGACGCTTAAAGACTAGGTGACTTTGGCAACACACAAGTGTAGTATA
ATTCTTTGCTTCTGCTTCTTTTGAATTTCACTGTTTAGATTTGATTTTAACTGAGAAATCACTGAATGTGCTCAG
TAATCATTTAGCAGGAGATTTTTGTGTCTCAACGAAATTTTCTCCATGGCCCCAGGGTATTTCTGTTGTTTCT
CCTGAAATTTCTGCTTTTGTAGTCAAGTATGAAACTCTGAACAGTAGATGTTTATATGGCAAAATGCAAGA
CAATCTATAAGGGAGATTTTAAAGATTTTGAAGTGAAGAAACAGATGCTACTGAGGGGCTTTATGGACCATCCA
TCAATTTCTGAAGTCTGACTCTCCCTTACCTTTCCCTGGTGTGCTCAGAACTCCAGGCTCACTGGAAGTGTAGT
GGAATCATGTAGTTGAATTTCTTACTTCAAGACATTTGATTTCTCTCCAGTATCAAAACATTAATGATCTTTTA
TGCTTTTTTTTTTTTATTTGTTATATCTTTAAGTTCTGGGTCACATGCTGCGCAACATCTAGGTTTGTATACATAGT
ATACATTTGGCCATGCTGTGTTGCTGCACTCATCAACCTGTCTCTCATCTTCTTTATGCTCTGTCTTTCAAGCA
ACACTCTGTTCTTCTGAGTACTGAAATCAGGTCACTTTACCACAGGCTCCATTTTAAATATGCTTCAACCTC
ATCCAGCACCTACTTAAGATTTATCTAGGCTCTGTGGTGTATTTAGACCCATAAAGAAATTTATGCTTCC
ATATGTTTGGTTACAGATGGAAATGGGAATGTTGAAGCAGATGAAGAAAGGATGTTTACATATTAAGCATCA
GTTCTGAAGCTAGATTTGCTGAGTTTGAATCTTAGCTCTTCCCTTTATAGCTCTGTGACCTGAGCTAGTATCA
TTAAATGCTCTGATCTCTTATTTCTGATCAGTGAACCTCCCTATTTCAATGTGAGAGTTTAAATTAATGAG
GACACTTAAATTTGAGGAGCTGATAGCATGATGTTTCACTACATGTTAAATGTTGTTTTTTATTTATGTA
CAACATCTGCTGGGACAGAAATTTAAATCATCTCAACTTTTGAAGAAATTTGAGTTATCAACACCGTTCCAC

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FIGURE 61B

AAGACAGTGGC AAAATTAFTGSGTGAGAAATTAACAGCTGTTTCTCAGAGGAAGCAATGGAGGCTTGCTGGGATA
AAGGCATTTACTGAGAGGCTGTTACCTAGTGAGAGTGATGAATTAATTAATAATAGTCGAATCCCTTTCTGACTG
TCTCTGAAAGCTTCCGCTTTTATCTTTCAAGAGCAGAATTGTACCCCCAAGGACATTTATTAATAAAAGAACAA
ACTGTCCAGTSCAATGAAGGCAAAAGTCATAGGTCTCCCAAGTCTTACCCCATTCCTGTGAAATATCAAGTTCTT
GGCTTTTCTCTGTCATGAGCCICAACTTTCTCCGACCGGCTGCATTTCTTTCTCTGGTTTCTAAATTGCCRG
GGCAATTTGGATCACTTACTTAATATCTGTTAAATTTTGTGACCCAAACAAAGTCTTTTAGCACTGTGGTGTCA
AAAAGAAAAACACCTCCCAGGCATATACATTTATAGATTCTTGAGAAATGTTGCTCTCCAGCTCCATCCCCAC
CCAATGAAATATGATCCAGAGAGTCTTGCAAGAGACAGGCTCATTTTCCACAATTAGCTCTAAAGTGCCCTCC
AGGAAATGATTTTCTCAGCTCATCTCTCTGTATTCCCTGTTTGGATCACAGGGCAATCTGTTTAAATGACTAA
TTACAGAAATCATTAAGGCACCAAGCAATGTCTCTGAAATACACACATCCCAAGCTTTACAAATCCTGCC
TGGCTTGACAGTGATGAGGCCACTTAACAGTCCAGGCGAGGCGGATGTTAAAAAAATTAABAAGGPGACCATCT
GCGSTTAGTTTTTAACTTTCTGATTCACACTTAACGTCTGTCATTCTGTTACTGGGCACCTGTTTAAATTC
TATTTTAAATGTTAATGAGTGTTGTTTAAATTAATCAGGAAGAGAGAGAAAAA

FIGURE 62A

[illegible]

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FIGURE 62B

CTATCAAATATATACTGAGCCTGTGTGAAGTATCTCATCAATTTCCAAAAGGAACACCTTGTGTGATGCCAG
TGAGCAATTTCTAAAAAGGGTGTGAGGTAGAGGTAAAAATAAGGTGAGAGACCATTTGAGANTGCACCTGTGTGCTC
AAAAAGGTGATCTGGTTCTTTCTTCAGAGATTTCTACGGGGATAGAAAATCGGGAGTCTGCCCTCAATTAATCTG
TGACTCCACCTCTTGCATCAANTCAATATCTATTTGTTGAGCACTTATTAATTAAGACCTTGCTATGTCTGTGTC
CATTTTGATTTGAGATACAACCTTTTTGTGTGCGSTTGAATGACAAATCACCTCCAAACAAAATGGGGCACAGAGAA
TCAGCTAGGAGACCCAGTTAATCAGGGTCCATTTCTCTTGATGTAAAGGAGTCTGGGTAAAATGTGGCTGTAA
CCTAAACCACTAGTCCTTGTGATTTGTTTCTGCCCTCTGTGTTTCTGTTGTCAATGCTAAAGTGTGTGTTT
GCAGTCATGAACCTAAAGCACAAAAGATGCATGAGACATTTGTAGTCATATGTCTGGTGTGACACTTTGGAGCAA
AAACCTTSCAGTGGTAAATAAAAAATTTCCACAGGGAAAAA

ASGCSGACGCTCCGCTGAAACATGCAATTCAGCCAGTCCCTCCGCACTTCTGGAGCGGGGACAGGCGCCAGSSGCATC
 AGGACGCAACCCAGGAGGACCTGGGAAATAGGGRTTCCTTCCCTCCACTTCAGGTTTTAGCAGCTTGGTGCTAAA
 TTGCTGTCTCAAATGCAGAGGATCTAATTTGCAGAGGAAACAGCCAAAGAGGAGAGGAGGAAAAGGAAAA
 AAAAAGGGGTATATTGTGGATGCTCTACTTTTCTTGGAAATGCAAAAAGATTATGCATATTTCTGTCTCTCTTC
 TCCGTGTTTTATGGGGACTGATTTTGGTGTCTCTTCTAACAGCATACAGATAGGGGGCTATTTCTCTAGGGCG
 CCGATCAAGANTACAGTGCATTTTCGAGTAGGGATGGTTCAGTTTTCCACTTCGGAGTTCAGAGTGCACACCCAC
 ATCGACAAATTTSGAGGTGGCAACAGCTTGGCAGTCACTAATGCTTTCTGCTCCAGTTTTTCGACAGGAGTCTA
 TGGTATTTTTGGATTTTATGACAGAGAGTCTGTAAATACCATCACATCATTTTGGGGAACACTCCAGCTCTCT
 TCATCACTCCAGCTTCCCAACAGATGGCACACATCCATTTGTCAATCAGATGAGACCCGACCTCABAGGAGCT
 CTCTTAGCTTGATTGAATACATCAATGGGACAAGTTTCATACCTCTATGACAGTGCAGAGGCTTATCAAC
 ACTGCAAGCTGTGCTGGATTCTGCTGCTGAAAGAAATGGCAAGTGAAGTCTCTCAATGTGGGAACATTAACA
 ATGACAGAGAAAGATGAGATGTACCGATCACTTTTTCAAGATCTGGAGTTAAAGAGGACCGGCTGTAAATCTG
 GACTGTCGAAAGGATTAAGTAAGTAACACATGTGACAGCGGTTATTACCATTTGGAAACACGTTAAAGGGTACCA
 CTACCTCATTTGCAAAATCTGGAATTTACTGATGGAGACCTATTAAAAATCCAGTTTGGAGGTGCAAAATGTCTCTG
 GATTTTCAGATAGTGGACTATGATGATTCGTTTGGTATCTAAATTTATAGAAAGATGGTCAACACTCGAAGAAAA
 GAATACCTCGAGGCTCACACACACAAATTAAGTATACTTCTGCTCTGACCTATGATGCCGTTCAAGTGTGAC
 TGAAGCTTTCCGCAACCTAAGGAGCAAGAAATGAATCTCCCGAAGGGGATGACGAGAGCTGTCTGGCAA
 ACCAGGCTGTCCTGGGACAGGTTGTAGAAATAGAAAGGCCCTCAACACAGTTTCAGTTGAGGCTCTCTCA
 GCAAAATATAAGTTTGACCAAGATGGAAAGAAATAACTATACAAATTAACATCATGGAGCTCAAACTAATGG
 GCGCGGGAAGATTGGCTACTGGAGTGAAGTGGACAAAATGGTTGTTACCTTACTGAGCTCCCTTCGGAATG
 ACACCTCTGGGCTTGAGAATAAGACTGTTTGTCTACCAACAATTTGGAATCTCCGTATGTTATGATGAAGAAA
 AATCATGAATGCTTGAAGGCCAATGAGCGCTATGAGGGCTACTGTGTGACCTGGCTGCAGAAATCGCCAAACA
 TTGTGGTTCAAGTACAGTTGACAATTTGTTGGTATGGCAATGATGGGGCAGGATCGAGACAGAAATTT
 GGAATGGAGTGGTTGGAGAACTTATATGGGAAGCTGATATGCAATTTGCTCATTAACATTTACCTTGTG
 AGAGAAGAGTGGTGGTACTTCTCAAGCCCTTCATGAGCTCTGGGATATCTATCATGATCAGAGGCTCAGAA
 GTCCRAACCCAGAGTGTCTTCTCTTCTGATCTTTAGCCATGAGATCTGGATGTGATTTGTTTGGCTACA
 TTGGGGTCAGTGTAGTTTTATTCTCTGGTCAAGCAATTTAGCCCTACAGAGTGGCBACTGAGGAGTTTGAAGAT
 GGAAGAGAAACACAAAGTAGTGAATCAACTAATGAATTTGGGATTTTAAATAGTCTCTGGTTTCTCTGGTGG
 CTTTATGTGGSCAAGGATGCGATTTCTGGCAAGATCCCTCTCTGGGCGCATTTGTGGAGGTGTGGTGGTTCT
 TTACCTGTATCAATCTCCTCTACAGGCTAACTTAGCTGCTTCTCTGACTGTAGAGAGGATGGTGTCTCCC
 ATCGAAAGTGTGAGGATCTTCTAAGCAACACAAATTTGCTTATGGACATAGACTCTGGCTCCACTAAGAA
 GTTTTTCAGGAGATCTAAATTTGAGTGTGTTGATAAATGTGGACCTACATGGGAGTCCGAGGCCCTCTGTGT
 TTGTGAGGACTACGGGCCAAGGGGTGGCTAGAGTGGGGAAGTCCAAAGCGAAATATGCTACTTCTTGGAGTCC
 ACGATGAACGAGTACATTTGACCAAGAGGCCCTTGGCAGACCATGAAAGTGGGTGGAAACCTGATCTCAAGG
 CTATGGCATTCGCAACCTTAAGGATCTCTCATTAGCAACCCAGTAATATTCGAGATTGAAACTCAGTGAGC
 AAGGCGCTCTTAGCAAGCTGAAACAAATTTGTTGCTACGATAAAGGTGAATGTGGAGCCAGGACTCTGGAAGT
 AAGGAAAGAGACCACTGCCCTCAGTCTGAGCAACGTTGCTGGAGTATTTACATCTCTTCTGGGGGCTTGGTTT
 GGCANTGCTGGTGGCTTTGATTGAGTTCTGTTACAGTCAAGGGCCGAGGGCAAGAGATGAAGGTGGCAAGAA
 ATGCAAGAAATTAACCCATCTTCTCTGACAGATTCACAGAAATTTGCAACTTATAAGGAAGTTACACAGTA
 TATGGCATCGAAAGTGTAAATTTAGGGGATGACCTTGAATGATGCCATGAGCAACAGGCAAGGCTGTCAAT
 TACAGGAAGTACTGGAGAAATGGAGCTGTTATGACTCCGAAATTTCCCAAGCAGTGCATGCTGTCTCTTACG
 TGAATCTGGCATGGGAATGAATGCTGAGTGTGATGATCTCTGTTGATGATAAGAACCTTTTGAAGTGCCTTAC
 ACAATGGTTTTCTGTGTGTTTATTGTCAAAGTGGTGAGAGGCATCCAGTATCTTGAAGACTTTTCTTACAGC
 AAGAAATCTTAAATATCTGGAGTTTCACTTGAATTTGAAGGAATGATTAATTAAGACACAACATCTTTTCTAC
 TCGAGTTACAGACAAAGCGGTGGTGGACATGCACAGCTAATCAGGAAGTACATATAATTTACCTGAAGTCTTTGTA
 CAGACAAACAAACCTGTTTCTGCAAGCACTATTGTAGTCTCTTGAATCATATGACTTAAAGCACTTGCACATC
 AACTGCAATCAAGATGTGACATGTTTTATAAAAAAGAAAAAAACATTTAAAGATAAAAATATTTTTAGGTA
 TTTTCAACAAACAACTGGCTTTTAAATAAATTTGCTTCCATATTGTTGAATAAGCAAAAAACATTAACCTGA
 GTGGGAAGTGAATAAAAAAGGCTTTAGGTATCGATTTCCATATTTTTCAAAGCCAAATATGTAATGCTAAGGA
 AAGTAAACAAAGAGGAGATTTCAATCTTGTAATTTATATTTGTTATTAAACCTTAAATGTATCTTCTTTAA
 CATTTGGTGTAAATATAAATTTACTTGGCAATGGCTGACATTTGAAATAAACATTTTCTATTTGTTTATTTGA
 ACTGGTCCAATTAATTTTGTCTAGCTACAGTTTGGTGCATAAATCAAGTGAAGTTAAGCACTACCAAGTTGTT
 AGGTGCCGACAGAGAAATTTCTCCCTTTTAAAAAGGCCAGGTGATTTTTCAATGTATCTTTGCCCCAAGTAA
 TATCCGAATATCTTTTGACATGCTTAAATATATATATATAAAGAAATATTTGTTAAACAAAGCATTTGA
 TCTATGTAGATAAATGCTAATAGATTTAAAGGCTAATATTAACAAATACAGAAATAGCTGAAGTTCCATTTT
 AAAGTGTTTGAGCTTACAGAGAGAAACATTCATTTAATGAAGTAAAAATGCCCTTGAAGTAATTCCTTAC
 ATAGTTGCCCATTGATTAAATTTCAAAAACTAATATGTTTTAGCTTTTAAATTAAGAAAGCTGTCAATACT
 TTATATATTATGAATTTTAAATATGTTTGAAGTCTCCGCAATATAGTTTTCTCCATGACATGATTAATAA
 TAAACCTTAATATATTTATTTTATATTTATCTCAGGCGGAATGGCTATTTTTAATATGCCAGTGTGGATAAA
 TGTCACTTTCTGTAACTTTTGAATAAGAGGCTATATTTATCTAGTTAATGAATTTAAAGGATCTATCTTTCC
 CTTCATAAATAACCTCTTATTTCCATTAAGGCCCCCAAGTTTAAATTAATTTAGGATTTTGAATGATTATGAC

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FIGURE 63B

ATCCAATAGTTATTTTAAATATTTGTATTCTTGTATTCTGGAAGARAGCCTTGTGTAGCACTTGGTATTTT
GCAGAGTGCTTTTAAAACATTCTTACTTACCGTATTTTCATAGAGGGGAGGAAAAATGTAAGSTTTAACAGTAA
GCCTTGGCATTGAACATGGAGCCATGTGGTATCATGATATCTTCACTAAATTTAGCTGTCCCTAATCACAGAT
CCTAAGCTAATATAATATAATTTTAGTGCAATTTCTCCCTCAFCAGGAATGCTGGAGGTGCATTTTAAGTTTTANT
AAIAAGTCTAGAAATGACCAARTTGCAGACTAATTTGTTTCCATATTTGTACTTAAAATGAGTTTTAABAGTGAA
AAAGAAATGACTATATACAAATCAATGCTATTTATTGTACCTCTGGGCCCTACTCTTCTAAAAATTTGTAGCTTATC
GATTTTTCTCTGTCAAGCTTGAACATAATGTAATAATTTGAATTAATGTAAGTTATATTTTCATGPTTTTATAG
ATACAACATGACAGGAATACATAATGTAAGAGTATTTCAACTATGGATAATGTTGATTGGATAATGCACATCTC
AGTTACAAGCAGTACTCATAGTTTAAATATOCATGTAACGGTGCATCAATATATTGCTATATRAATATGTCTGTG
TGCATATAAGTGAAAAGTGGTCAACCAAGAGTATGACAGCTGTCTAAAGGTTTTTTTATTTCATTTTATATAAA
AACTGTTATGCAAAAGCAAAAATGTTTATGAACATATCTTATGTAAATPTACAATTGTCCTTTACGTACTTTT
TTGTTTACAGTATAGTACCTTATTTTCTGCTGTGTTAAGTGGGTGTCMAACTCCAAGAAGACATACACTTTCTA
TAACITTCATTTGAAGATATTTGGAAATTTCCAATTTTTCATGTGTACTATGTCAGAAATGCTTTCCGATTTTATTT
TTAAATCTAACATCGGATGGCTTTTCCGGAGTGTTGTAAAACTTCAATCATACATAAAACAGTTCTTACAAA
AGGCRAAGATCTT

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FIGURE 64

GCCAACACTGGCCAAAAGGGATAGCTGTCCAGGCTCTCCCCAGCACTGAGGAGCTCGGCTGCTGCCCTCTTGC
 GCGCGGGAAGCAGCAACCAAGTTCACGGCCAAACGCTTGGCACTAGGGTCCAGAAATGGCTACAAACAGTCCCTGAT
 GGTTCGCCCAATGGCTGAAATCCAAGTACTACAGACTTTGTGATAAGGCTGAAGCTTGGGGCATCGTCTAGA
 AACGGTGGCCACAGCCGGGTTGTGACCTCGGTGGCTTCATGCTCACTCTCCCGATCCTCGTCTGCAAGGTGC
 AGGACTCCAACAGGCGAAAAATGCTGCTACTCAGTTTCTCTTCTCTGCTGGGTGTGTTGGGCATCTTTGGCTC
 ACCTTCGCCCTTCATCATCGGACTGGACGGGAGCACAGGGCCACACGCTTCTTCTCTTTGGGATCCTCTTTTC
 CATCTGCTTCTCTGCTGCTGCTGCTCATGCTGTCACTCTGACCAAGCTCGTCCGGGGGAGGAAGCCCTTTCCC
 TGTGGTGATTCTGGGTCTGGCCGTGGGCTTCAGCCTAGTCCAGGATGTTATCGCTATTGAATATATTGTCTCTG
 ACCATGAATAGGACCAACGTCATGTCTTTCTGAGCTTTCCGCTCCTCGTGGCAATGAAGACTTTGTCTCTCT
 GCTCACTACGTCCTCTCTTGATGGCGCTGACCTTCTCATGTCTCTCTTCACTTCTGTGGTTCTTTCAAGG
 GCTGGAAGAGACATGGGGCCACATCTACCTCAGCATGCTCTCTCTCCATTGCCATCTGGGTGGCTGGATCACC
 CTGCTCATGCTTCTGACTTTGACCGCAGGTGGGATGACACCATCCTCAGCTCCGCTTGGCTGCCATGGCTG
 GGTGTCTCTGTGGCTTATGTTAGTCCCAGTTTTGGCTGCTCACAAAGCAACGAACCCCATGGATTATCTG
 TTGAGGATGCTTTCTGTAAACCTCAACTCGTGAAGAAGAGCTATGGTGTGGAGAACASAGCTACTCTCAAGAG
 GAAATCACTCAAGGTTTTGAAGAGACAGGGGACAGGCTCTATGCCCCCTATTCCACACATTTTCACTGTCAGAA
 CCAGCTCCCCAAAAGGAATTCTCCATCCACGGGGCCACGCTTGGCCGAGCCCTACAAAGACTATGAAGTAA
 AGAAGAGGGGACGCTAACTCTGTCTTGAAGAGTGGGACAAATGCAGCCGGGGGGCAGATCTAGCGGGAGCTCAA
 AGGGATGTGGCGAAATCTTGACTCTTCTGAGAAACTGTACAAGACACTACGGGAACAGTTTGGCTCCCTCCC
 AGCCTCAACCACAATTCTTCCATGCTGGGGCTGATGTGGGCTAGTAAGACTCCAGTTCTTAGAGGGCGCTGTAGT
 APTTTTTTTTTTTTGTCTCATCTTTAGATACTTCTTTAAGTGGGAGTCTCAG

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FIGURE 65

TCATTCCATTAAACATATTTCTAAATAATAGTAAGTGGTACTAACAAAATAAATAAATTTAATAGCCTTAGA
AATAAATGACTGTATACCTTATACAGGTTGAAAAAACTCGGTAGGAATAAGTTACCTTTTTGTTTACTAATGTT
GGTTTCAAAAATACTCAGATTCATTTTAGTTGGCTGACATCTGGAAGTAGTTAACAACTAACCACTGGACTTCA
ACATCATTTGCTCCAGGCTTCCCCCATCATCACCTCACCACATATCCTGCTAATATCCAACAACAAACAAA
TATTTAATATTTGAAATAGCCCATTTGCCCTGAGAATGAACACAAGCTAAAATACATGCAAGGGTACTTAATGGAG
CCAAACCATGTTCTATACCTAAGGAGAAACATGGACATGTAGAATGCTTTTATTCAATGTAATCAAATCAGAA
CAATCAGTGTATATCACTAGAACATCAGATGGAGGATAACACAAGAAGTGATACAGATCAGGGTTCACTTCTC
TTACCTCTCTCTGTTAGGACCACATTCCTATTTTACCCAAATGTTTTCTGGTACGGGCCATCTTTTCACCATAA
ATGGCATATGTTTTCAAATGGCTAAAGCTTATTTATGGGTATGCTCAAAGGAGTAAAACCCCAATTCACAGAGAT
GTGGCTTTTCTAAAGAACCAAATTAAGGGAATACTTAGTATCTACAATAAAGTATTAGTCATTCTGAGGATTA
TTTGTTCCTTTAAGTATTAGCTCCCTACTACATCCATAACACCCCTACTTACTAAATTTAATTACACACAACCTT
TCAAGAATTGATTTTTATTTGAAGGGAGGTACCTGTCTACTTTATCTACAATAAAGTATTAGTATTGAGGATTA
TCTCTAATCCATGCAAACTACAAATTCATCGGGAGTCTTACATCACTAACAGTGGTATGAACAAAACCTAAGAA
AGTACTTCTATCCACATGTGAATGTTTTAAAAAAGTTTTTGCCATAAAACCTAAGTGTATTTAGCATACCAC
AGTGTCTCTGAAGATGGGTCAATGACGATGTACCATTTGTATATAGGTAATACACATGTAAATCACTAATTGTTA
ATTAAATATAAGAAGTAGGTTTTTATCTTTTTTAAHNAAAAAACAAAAAGGTGACTCCCTTTCTCATTCTGTTC
TGTTGTATTGCGTCCAAAAGTTGTGTGAATTTTTTTAAGGTCGAAGAAATGTAAAGAAATTTGTTGGAATACC
TGATTTTCTGTAAAAAATAAAAAATAAATAAGATTTTCTTACTT

[illegible]

FIGURE 67

[illegible]

[illegible]

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FIGURE 69

CAGGCGCTCTGAGGGCTCCCTTGCCGAGGGGCCCCGAGCTGCAGGGACAGTGAGCAGTGAGTCCCTTGGGCATCCCC
 CTCCTGGGCGAGGTCACCAATAGGTCCCCGCGAGTTCCCAATGGAAGTGTTCAGTCCCTCCCCGAGGGCTCCACTT
 CAACCTGTCTGTGTCTGTGCCAGGCGCTGGAGTTGTGTGACCCCTCCCCACCGCTGGCCTTCTCCATGGGGGCTGG
 CCTTTCTCGGTGGTGGGCACCCCTGCTGCTGCCCGGCTGGCTGGGCTTGTGCAGGACTGGCGTCTTCTGCAGG
 GGCTGGGTGCCCTGATGAGTGGACTGTTGCTGCTCTTTTGGGGGTTCCCGGCGCTTCTCCCGAGTCTCCCTGC
 TGGCTGCTGGCCACAGGTCAGGTAGCTCGAGCCAGGAAGATCCTGTGGCGCTTTGCAGAAGCCAGTGGCGTGGG
 CCCCCGGGACAGTTCCTTGGAGGAGAACTCCCTGGCTACAGAGCTGACCATGCTGTCTGCACGAGAGCCCCAGC
 CCGGTACCACTCCCCACTGGGCTTCTGCGTACCCGAGTCACTGGAGAAACGGGCTTATCTTGGGCTTCAGC
 TCGCTGTTGGTGGAGGACATCAGAGCTAGCTTCCGCCGAGCGCTGGCAGCTCAGGTGCCGACCTTCTACCTGCC
 CTACTTCTCGAGGGCGGGCTGGAGGCGGACGCTTGGTCTTCCTGCTCCGACGGCAGATTGCTGTGGACGGC
 GCGCGTGTCTGCTGCTGGGACCAATGGTFCACAGGCGCTGGCATCCCTGCTGCTCCTCGCTGGGGCCAGTATCTG
 CCAGGCTGGACTGTGCTGTTCTCTCTGCTCCTGGGGCTCCTGGCGCTCCCGGCTGTGTCCGCACTCAGCAGGCT
 CTTCCGCGCCGAGGTCTTCCCCACGGTGATCAGGGGGGGCGGGCTGGGCTGGTCTGGGGGGCGGGTTCTTGG
 GCCAGGCAGCCGGCCCCCTGGACACCTGCAAGGCGGGCAGGGCTTCTTCTTCAACAAGTGGTCTTCCGCTCC
 CTTGCTGTCTTGGCCCTGCTGTGTGTCTGCTGCTGCTGAGAGCCGAGCCGGGGGCTGCCCCAGTCACTGCA
 GGAAGCGGAGCCGCTGCGCCGCTCCCACTCCTGCGGGGCGGCCCCCGCCAGGACCACTGCTCTGCTGCCGC
 CCTCCAACTCCTACTGGGCGGGCCACACCCCCAGCAGCACTAGTCTCTGCTGCTGGTGGCGCTGGGAGCCAGGATG
 GGACCAAAGTCAAGGCTTGGGGCATGGCTGAGTACCCAGAGCTCTGGTCCAGGGCAGACACATTCCTCTCAGA
 AGCCCCGTGCTCAGTGCAGGTGGAGCCGTGGGGACAGCGTGAAGGTGTCTCCAGCCAGGCCCCAGGCACTGGGA
 GGCCCTGGGTCTCCCCCAGCCACACCCAGTAGGTGTGGAGGATAAAGGCTTCTGTGGAAGTTGGCGTCTCTCC
 TGGTTCTTCCCTCAGGCCCACACCTGGGGCTGGAGGGTCTCACCTGTGCTGCTCCCCACCTCTGGGGCTCAC
 AGCAGGAGCCAGGGTGTGAGCGGCTGCTCCATAGCCCCCTGTCCAGGTAGTGGCAGCCCCCGGCGCGCTCTG
 CCCAGCCAGCAGGGTGGTATGGGGGCTGGCCCTCAGGTCCCTGCCAGGCCAGGCTCACTGGCCCCATCCCC
 CTCATGGTCAGTGTGGCAGTGGGCGCCGCTCCTGCATGAAAGAGACTAGCAAG

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FIGURE 70

AGCGGGGGGGGGTCCCGAAGCCCAAGTACCAGACCTCCTGTGCGAAGAGTAACCTGCTCTTCGGACTGATAAAGT
 GATGGGAATGGCCCTTTAGAAAGGGGAGCATCTTCAGRATCTGCAGCTGGGATCAGATTGTTCTTTTGTGTAATCAA
 CTCAGCTCTGCCAGCCAGCATCTTGCTAAGGGTTACAAAATAAATGCCATTTGAACAGTGCCATCTGTCATGG
 AAAACCGTGAGACGTTTTGTACAATGCCGTGTCTAAGGAGCTGGTTGGAGASTTTTGGCAATTTGTTCAACTTGA
 TAAAGAGGCCTCTGATCCTTTACGCTAAATGAATTAAGATTAGATTGAATATCAASGAAACAGAAAGAGAAATTAT
 GGCAAAGGCTGAAGAAATTTATTGACAGATGTGTTGTTTGAAGAGCCCACTGGATGGGTGGCAGGTAGTGGAGCC
 CAGGGTGAASACAATATGGAAACCAACATGGCTCAAAAATGAGAAAGCATAGAAATATTTATGCAATTAC
 ATCTGTGATTTCTTGCTTCTGTGTCTGTAATAAATGAAGTGAAGAACTACGAAGCCCTACTGGAAATGTGTFATTA
 TATTAAATGCTATTTTATATGCAATTACCTGAGTCTGAACGAAAGCTACAGACTTCTATTCAGGATTTGTGTGTT
 ACCGTGGTGGGAGAAAGCCCTGCCTGCCAGGAAGACACAGGAAGACAGCCCTTTGTCTATGTTACTAAGGAGGAG
 TCTGGAGACTAAGACAGGTGCAGACATCTGCGGCTTTGGCCTATCCATCAAGCTTTATATTGCTTTGATTTATG
 ATTTGGAGGAAAGTGGAGAAATTAAGATATGTTACTTGAAGTCTTCAACTGGAATATCAACTTCATCAAAATGATCCACGGGACCATTA
 AAACCACTTACAGGGGATTACAAAAGTCTTTGATGGTATACATTCAGAAATTTATTTTCAGAGCTTGGAAAAAGG
 CTTACGGGAAATTAAGTGGAGGCGATTTGAAATGATTGCAATCCAGGACTTCATGTTCCACGGGATACACCTTCCG
 AGGAGTCTCCAGTGCATTTCCAAAGTGGGGAGGTTCTGAGTTACTTTCCACCTCAAAAGAAAGTTCCGAGGG
 AGTGGAGAGATGCTTTATAGATTATATAAGCCCATCCTTTGGAGAGGATTAAAGGCCAGAAACTCTGAAGTTC
 GATCAATGCTGCAATTTGTTTGTGTTGAAGCTTTCCATTAGGGATCCAAAGCTTCATGCTATTGAATGGAT
 AGTAAATCCAGAAACAGTTTGAAGAGCTCTATAGCCCTTTTGAAGATCCTTACCGGATGGTCCGTTCCACAGG
 GATCCTTGGGTCTTTGTAATAAATCTTAAAGTACTGGGAAATGATGCCCCGACCATTTATTTGACCTCTGSA
 AGAAGGTGACTGGGGAACTGGCATTTCACACGAGCTCAGCTGATGTTGTTGTTCTGTTCTTTAAGTGTCTGCCA
 ATGATTTTGGACAACAACTGAGGCCACCATTTGTTAGAGCAAGCTCCTTCCAGCTCTCAGATACAGTCTCCACGA
 CAATTCGGAGAAAGTGAAGGCTAGCTTTTGTGGACATGCTGTTGAAGATCAAGCTCTGAGGGCTGCTAAGTTTT
 GGAATAATGTCCTTGGAGCACATTTCTGTTCTGTTGGAATCAGCCGAGGAGGTCTGTTGCGAGCCCTGTGTCCACCTGGT
 AGCCTCATCTTTAATTTCTTCCCTGCTGGAATCAGCCGAGGAGGTCTGTTGCGAGCCCTGTGTCCACCTGGT
 GCAGATGCAACACGCGGCTGCCAGGAGGTTCTATCAGTACGCCCCAGAACACACCCGCTGCACCAACATAGCAA
 AGCTGATTCACGTTATTCGTCATTTGCTTAAATGCCGCTATCCAGAGGGAGTGAAGAGCCCTCCAGAGGACGAG
 GAGGAAGAGGACGGAAGGGAGAGGAGGAAATGTGACTGTTCTGGACAAAACACTGTCTGTAACGATTTGTGCAATG
 CATGGCAGGTTTACTAGAAATCATTTGCTATTTCTCTGGAAAGTATTGACAGAGTATCTGAAAGTATTTAAGGATGATCGCTGC
 CCAAACTTTACAGGATTAACAAATTTGCTCTGTTGCTTCCAGAGTATCTGAAAGTATTTAAGGATGATCGCTGC
 AAGATCCCTTTATTTATGCTAATGTTCTTTATGCGGCTCTGCTGTCCCCCATTCAGCTGTGGTGTGATTTTC
 CACGCTGAGAGCCCGGAGGAGGGGCTGTTGGACAGAGCTACGCACTTTGTTGGATTGCTCTGCTCTGCTGGG
 GCGAGGTGGGACATTTCTGGAGCTTGTGACAAGTGGCTGCCACAGAGCATGCCAGGCGGAGAGCAACACA
 GCTTCTAAGAGGTAGGGTGCAGATCCATGACACAGCCGAGTCAAACTGAAATTTGGATTGCTCTGATGAGTA
 TCTGCTGACTCATCAAAAGAACCGAGAGTCTTCTCTCTGCTCTCGGAGAAAGTCAAACTTAAACCATCTTTGAAAG
 CCCTTGAAACGTCARAGGCAGATCTGAGTCACTCTGTCAGACACCGGGTGGGAAGCCTCGTGGCTTCAGTGAA
 GCAGCTGCCCGGAGCCTTTGGTCTCCACTGTGCGCTGAGCATCCATCTTCAGCACAAGTTCTGCTCAGAAAG
 AAAGGTGTAATTTGCTCCTGTTGGAAGACACTGGCTTTTGGTTAGAAAGCAAAATTTTATCTTTTATTCAGATC
 AAGAAAGAGACTACCTGAAGCTTCTATAGGCTCAATTTATCAGCAAAATTTATCCAGACCTACCTGACTGTGTGTA
 GATGTTGTTATGGTAGGCTTGGTGACCATCAGTTTTCAGATGCACTCTTACAGCGGAGCTCTTGAATCATGCA
 AACAGTGAAGGATTTTTTTATGTTTCAATTTCTTCTGACATTTGAAAGAGATAACTGGAAGTCTCTGATTC
 AGAAACAGATTTCAGATGAAGAGTTGCAATGCTGTTGGACACAGTCCAGAAAGTATTTTCAGAAATGTTGGAA
 TGTATTTGCACGAGCTTTCAGGAAGCAGCCGAGAGAGGCTGCGGCTGCTTATTTCTGTTTCAGAGGCTCTTCA
 TGAGTTTCATTTACTGCTGTTCACTCTGCGCACACAGACACCCCTGTGCAACCGGGGTGTTACTTTCTACTCTGATCG
 CTGGGCTGTGTTGAGATAAGTCAACAGCTACGGAAGGTTTCTGACGTAGAAGAGCTTACCCCTCCAGAGCAT
 CTTTCTGATCTTCCACCATTTTCAAGGTGTTTAAAGCAATAAATAAAGTCTTGAAGTGTGCTGAGGTCATTT
 TTTGGATGAATTAAGGCTATGTTGCTTCAATGATATTGAAGGCAATTTGCTGCTCAGCGCTGCTGTGCATA
 TTATCCCTGTTTATTAATGCAGGTAACATAAAGCTCAAAAGTGAAGGAGGTTTCAGGCCACTGTTTCAGAGAAA
 CTAAGACATTTCAAGAAATTAATTTGGAGAGGATATCATTGAAGATTTCTCTATGAATCATCATCAAGAAC
 TCTGGGAGAACTTTTGAATTCATAAAGGCAACATCTCCAGACATGTAATAAGGGGAAAGGATTTCAAT
 TGAATGCTGTTGTTATTTTCTATTTGTTTTTAAATGTTAATAACCCATATAATAGGGGAAAGGATTTT
 GTGGGAATGTGGGAAGCTGGGGGTTATGGAGGAGATAACTCAAACTTCTTCAATTTTGCCTAGTGCCTGCGTA
 AATAATATATTTATATAAAGCACTCCAGGATGAAATGGTGTAGAAATCATGATTCCAGAAAGAACACTTT
 CTAGCAACCTGTTGTTTTTAAATGACTTTTATATATGTAATATTGCTTGGAAACTATGAGTAATAAGCAA
 TGACARCAAMAAAAA

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FIGURE 71

GCGCTTCAGAAATCTGCAGCTGGGATCAGAAATTGTTCTTTTGTGTAATCAACTCAGCTCTGCCGASCCAGCATCTT
 GCTAAGGGTTACAAAATAAATGCCATTTGAACAGTGGCATCTGTCAAGGAAAAACGTGAGACGTTTGTGACAAGC
 CGTCTCTAAGGAGCTGGTTGGAGAGTTTTCGAATTTGTTCAACTTGATTAAGAGGCCTCTGATCCTTTTCAGCC
 TAANTGAATTAAGATGAATTTATCAAGGAAACAGAAAGAAATTTATGCGAAAGGCTGARGAATTTATTGACA
 GATGTGTTTGTAGAAAGCCGATGGATGGGTGGCAGTATGGAAGCCACGGSTGAAGACAATATGGAAACCGA
 CATGGCTCAAAAATCAGAAAAGCATAGAAATAATTTATGCAATTTACATCTGTGATTTCTTGCTCTGTGTCTG
 TAATAAATGAAAGTGGAGAACTACGAAAGCCCTACTGGAATGTGTTATTATATTAAATGGTATTTTATATGCATTA
 CCTGACTCTGAACGAAACCTACAGAGTTTCTATTCAAGATTTGTGTGTACCTGGTGGGAGAAAGGCTGCTGC
 CAGGAGAGACACAGGAAGACAGGCTTTGTCATGTTACTAAGGAGAGCTCTGGAGACTAAGACAGGTCAGAGC
 TATGTGCGGCTTTGGCGTATCCATCAAGCTTTATATTTGCTTTGATTTATGATTTGGAGCAAACTGGAGAAATTA
 BATAATGTTACTTTGAGTGGCTTCATATAATTAATATATCAAGAAAGAGAGGAAAGAAATTTCTGATGTCT
 CTTCAACTGGAATATCAACTTCATCAAAATGATCCACGGGACCAATTAANAACAGTTACAGGGAATACAAAT
 CTTTGTGATGGTATACATTCAGAAATTTATTTCAGAGCTTGGAAAGGCTTCAGGGAAATACTGGAGGCGATT
 GAAATGATTGTCATCCAGGACTTCATGTTCCACGGGATACACCTTCGAGGAGGCTCTCCAGTSCATTCGAAAGT
 GCGGAGGCTTCTGAGTTACTTTCCACCATCAAAAGAAAGTTCCGGCAGGAGCTGGAAGAGATGCTTTATAGATTAT
 ATAAGCCCATCTCTTTGGAGAGGATTAAGAGCCAGAACTCTGAAGTTCGATCAAAATCTGCAATTTGTTGTTGTT
 GAGCATTTCTCTATTAGGAGTCCAAACCTTCATCTATTGAATGGATAGTGAATCCAGAAACAGTTTGAGAA
 GCTCTATAGCTTTTGAAGATCTCTTACCGATGGTCCGTTCCACAGGAGATCTTGGTGGTTTGATAAAATACAT
 CTAGTACTGGGAAATGATGCCCCCGACCATTTCTTATTGACCTCTCGAAGAAAGCTGACTGGGAACTGGCATT
 GACAGGAGCTCAGCTGATGTTGCTTGTGTTCTTAAAGTGTCTGCCAATGATTTTGGACAACAACCTGAGCGA
 CCAATTTGTTAGAGCAGCTCTCTCCAGCTCTCAGATACAGTCTCCACGACATTTCCGAGAAAGTGAGGTTAGCT
 TTGTGACATGCTGTTGAAGATCAAAAGCTGTGAGGCTGCTAAGTTTTCGAAATATCTTCCATGGAGCACAT
 CTGCTTCTGCTCGGAAAGCTGATTCCTGACCTGTGCTCTCGGCGCTGCTGAGCTCATCTTAAATCTTTCTGCGC
 TGTGATCAGCAGCGGAGGCTCTGCTGCGAGGCTGTGTCTACCCCTGGTGCAGATGAACCAAGCCGCTGCCAGGA
 GCTTCTATCAGTACCCCCAGAACACACCCGCTGCAACCACTAGCAAGCTGATTCAGCTTATCTGCTCATTTG
 TTAATGCTCTGTATCCAGAGGGCAGTGGAGAGGCTCCAGAGGACGAGGAGGAGAGGAGCGGAAGGAGCAAGGA
 GATGTGACTGTTCTGCACAAACACCTGTCAGTAAACGATGTTGCATGCTAGGAGGCTTACTAGAAATCATTT
 TGATTTCTCTGAAAGATATTGACAGAGTATGGAATAATTAAGAGAGGCCAAACTTTACAGGATTAACAAGTT
 GCTCTCTGCTCTCCAGAGTATCTGAAAGTATTAAGGATGATGCTGCAAGATCCCTTTATCTCATGTAAATGTC
 CTTTATGCGCGGCTCTGCTGTCCCCCATTTCAAGCTGTGGTGTGATTTCCACGCTGAGAAGCCGGAGGAGGGCG
 CTGTGGACAAGAGCTACTGCACTTTGTTGGATTGCTCTGCTCTGCGGCGCAGGCTGGGGCACATTTCTGGAGCTT
 GTTGACAACCTGGCTGCCACAGAGCATGCCAGGCCAAGAGCAACACAGCTTCTAAGGAGTGGGTGCAGATCCA
 TGACACAGGCGCCAGTCAAACTGAAATGGCAATGGTCTACATTGAGTATCTGCTGACTCATCCAAGAAACCGG
 AGTCTTGTCTCTGCTGCTCGGAAGAACTTAACCATCTTTGAAAGCCCTTGAACCTGCAAGGACAGATCTG
 GAGTCACTTCTGCAGACACCGGCTGGGAGGCTCTGGCTTCAGTGAAGCAGCTGCCCCGAGGCTTTGGGTCT
 CCACCTCTGCGCTGAGCATCTATCTTCAGCACAGTCTGCTCAGAGGAAAGGCTGATTTGTCCATGTTGGAG
 ACACTGGCTTTTGGTTAGAAAGCAAAATTTATCTTTTATTCAAGATCAAGAAAGAGACTACCTGAAGCTTCAT
 AGGGTCAATTTATCAGCAATTTATCCAGAGCTACCTGACTGTGTGTAAAGATGTTGTTATGTTAGGCTTGGTGA
 CCATCAGTTTCAGATGCAACTCTTACAGCGAGTCTTGAATCATGCAACACAGTGAAGGGATTTTTTATGTTT
 CATTACTCTTTGACATTTGAAAGAGATAACTGGAATTTCTTGTATTCAGAAACAGATTCAGTGAAGAAAT
 GCAATGCTGTTGGACAGACTCCAGAAAGTATTCAGAAATTTGGAATCTATTGCAAGGAGCTTCAGGAGCA
 CCGGAGTCAAGGCTCGGCTGCTTTATCTGTTTCAGAGGCTCTTCATGAGTTTCATTAAGCTGTTGAGTCTC
 GGCACACAGACACCCCTGTGCACCGGGGTGACTTTCTACTCTGATCGCTGGGCTGFGGTTGAGATAAGTCAC
 CAGCTACGGAAGGTTTCTGAGCTAGAGAGCTTACCCCTCCAGAGCATCTTCTGATCTTCCACCATTTTCAAG
 GTGTTTATAGGAATAATAATAAAGTCTTCGAATGGGGTCAGGTCATTTTGGATGAATTAAGGCATSTGTGG
 CTTCTAATGATATTGAAGGCATTTGTGTGCTCAGGCTGCTGTGCATATTATCCTGGTTATTATGCAAGTAA
 CRTAAAGGCTCAAAAGTCAGGAGGCTCAGGCACTGTTACAGAAACCTAAGAGCAATTCATGGAATTTACTTT
 GGAGAGGATAGCATTTGAAGATTTCCTATGATCATCATCAAGAACTCTGGGAGAACTTTGAATTCATTAAC
 CAGGCAACATCTCCAGACATGAAGGGC

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FIGURE 72

TCCAACCAGATTTTCACCGCTATGCCTCCTTTCACTCTGGGAGTCTTCCAGAGGTCTTGCCTCGGGAGAGCAT
GCTCAGGTTTCCCCAGCTCTACAAAATCAGCCAGAAATGCCAAAGACTTCAACGTGAACAGTGGTCATGCCACTG
CCTGTTGATTTGTTGAAAATATTTGTTTACACGTATGTTCTTGTACTGATTGTCAGAAAGCTGGTPTTGAGACT
GCAGCTTGGACTAAATTCAGTCATCTGGCTGTCTGGGGAAGCATGCTGACCAGTCTGGTGTTCCTTGGCATCTA
CTCAGCCATCTGGTCCACCATTTCTCATTGCCCCAAATATGAGAGGACAGAAAGATGGTACCGGTACTGCCAATG
GAGATGGAGGAAGGAGACAGAAAGAAACAGAGCCCAGACCTAGGGACCACCAGCATTGTCAGAAATGGATAAAC
AGCCTTCTTCCTAACAAGGAAGCACAGCAACTGTGATCCTGAGCTGTGCACACTTCTGGTTGGGATTATTTCT
GGTTTCTACTTCTGTTTGAAGATGTGGCATGGAGAGTGAACAAGCTGCTGCCCCACCACCTGGCATCACAGCCC
CAGAACTCAGCTATTTCCATGGGACCCACAGCATCTCATCTCTGGGCTGAGCCAGAAAGACCCCTACTGAAGTCC
AGAGGCACTTTTCTGAAAGGCTCTGCTTTGACCTGAAGTATTTTATCTATCCTCAGTCTCAGGACACTGTTGAT
GGAATTAAGGCCAAGCACATCTGCAAAAAGCAATGCTGGAGGAGGTGCAAAAGAGCTGGAAACCAAGTCTCCA
GTCCTGGGAAAGCAGTGGTATGGAAAGCAATGGAAAGAGCATTGTAAGAAATGCCAATCCACTGTTTTCTGGC
CTTTATGATTTCTGCTGAGAAATCCACTGTTAGTCTGATGGGGTCTCCTTCATAGCAACCAATGACCTGAGAGC
CTTGTGAGGAAGACTCCATCTGATGACTCAGAGCAACTATTTTTTAGTGTGTTATTGTTATTAGCAGAAAGA
GGCCCTAATAATACATGGGGCAAGCTGAATATATCTTAGGCARAAGAAAGAAATATTCAAATTCCTATGTTATT
TTATCTAATTATTTATCTCTTTTTGTGTGTGACTTATAATGTGTCTATTGTATTAAATAAAAGTATATAACAT
GTAGTTT

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FIGURE 73

CATTCCCAACCTTCCTTCTTTAATAAGCAGGAGCGRAAAGACAAATTCCAAAGAGGATTGTTTCAGTTCAAGGG
 AATGAAAGAAATTCAGAAATAATTTTGGTAAATGGATTCCAATATCGGGAATAAGAATAAGCTGAACAGTTGACCTG
 CTTTGAAGAAACATACTGTCCATTTGTCTAAAATAATCTATAACAACCAAAACCAATCAAAATGAATTCAACATT
 ATTTTCCCAGGTTGAAATCAFTCAGTCCACTCTAATTTCTCAGAGAGAATGCCCCAGCTTCTGGCTTTTGAAA
 ATGATGATTTGTCATCTGCCCTTGGCCATGATAATTTACCTTAGCTCTTGCTTATGGAGCTGTGATCATTCTTGCT
 GTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGAGATGAGAAATGTTACCAACTCTCTGAT
 TGTGAACCTTTCTCTCAGACTTGCTTCTTGCCATCATGTGTCTCCCTTTACATTTGTCTACACATTAAATGG
 ACCACTGGGCTCTTGGTGAGGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTCAATCACTGTGTCCATT
 TTCTCTCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCCCTCGAGGGTGGAGACCAATAATAG
 ACATGCTTATGTAGGATTTGCTGTGATTTGGGTCTTGTGTGGCTTCTTCTTGGCTTTCTGATCTACCAAG
 TAATGACTGATGAGCCCTTCCAAATGTAAACACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTT
 CCATCGGACTCTCATAGGTTGTCTTATACCACTCTCTCTTGGTGCTGCAGTATTTTGGTCCACTTTGTTTTAT
 ATTTATTTGCTACTTCAAGATATATATACGCCCTAAAAGGAGAAACAACATGATGGACAAGATCAGAGACAATA
 AGTACAGGTCAGTGAAACCAAAAGAAATCAATATCATGCTGCTCTCCATTGTGGTAGCATTGTGAGCTGTGCTGG
 CTCCCTCTTACCATCTTAAACACTGTGTTTGATTTGGAATCATCAGATCATTTGCTACCTGCAACCAACAATCTGTT
 ATTCTCTGCTCTGCCACCTCAGAGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCTGAAACAAA
 ACTTCCAGAGAGACTTGCACTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGATGATGATTTATGAAACAATA
 GCCATGTCCAGATGCAACAGATGTTTCCAAACCTTCTTGAAGCAAGCAAGCCAGTCCGATTTAAAAAAT
 CAACAACAATGATGATAATGAAAAAATCTGAAGACTACTTATAGCCTATGGTCCCGGATGACATCTGTTTAAAAA
 CAAGCBAACCTGCAACATACTTTGATTACCTGTTCTCCCAAGGAATGGGGTTGAATCATTTGAAATGACTA
 AGATTTTCTTCTCTGCTTTTACTGCTTTTGTGTAGTTGTCTATAATTACATTTGGAACAAAAGGTGTGGGCT
 TTGGGGCTCTTCTGAAATAGTTTGAACAGACATCTTTGAAGTSCPTTTTGTGAATTTATGCATATAATATAAA
 GACTTTTATACTGTAATTTATGGAATGAAATTTCTTTAAAGTATTACGATCGCTGACTTCAGAAATACCTGCC
 ATCCAAATACGGTCATTAGATTGGGTCATCTTGATTAGATTAGATTAGATTAGATTGTCAACAGATTGGCCATC
 CTTACTTTATGATAGGCATCATTTTAGTGTGTTACAATAGTAACASTATGCAAAAGCAGCATTCAGAGACCGAA
 AGATAGCTCTTGAATCATTCAGAAAGTGGTTTGAGGTTTCTGTTTTTGGTGGTTTTTGGTTTTTTTTTTTTTT
 TTCACCTTAAGGGAGGCTTTTCATTTCCTCCCGACTGATTGTCTCTTAAATCAAAATTTAAATGAATAAAAAG
 ACATACTTCTCAGCTGCAAAATATTATGGAGAATTTGGGCACCCACAGGAATGAAGAGAGAAAGCAGCTCCCCAAC
 TTCAAAACCAATTTGCTACCTGACAACAAGAGCATTTTAGAGTAATTAATTTAATAAAGTAATTAGTATTGCT
 GTGTCAGGCTTCTGGTCTAATAAGTACTCGAAAGACTTTCCGCTTACAAATTTGTAGAAACACAAATATCGTTTT
 CCATACAGCACTGCTATATAGTGAATGATTTTAACTTTCAATGTCCATCTTTCAAAGGAAGTAACACCAAGGT
 ACAATGTTAAGGAATATTCACTTTACCTAGCCAGGGAATAACACAAAACCTGCAGATACTTCATATAGCCCA
 TTTTAACTTGTATAACTGTGTGACTTGTGGGCTCTTATAAATAATGCACTGTAAAGATTACTGATAGTTGTG
 TCATGTTAATGTGCTAATTTCAATGATCTTGTAAATCATGATTGAGCCTCAGAAATCAATTTGGAGAACTATATT
 TTAAGAAACAGACATACTTCAATGTATTATACAGATAAAGTATTACATGTGTTGATTTTAAAGGGCGGACA
 TTTTATTAATAATCAATATTGTTTTGCTTTTTCTGAGGAGTCTCTTTCAGTTTCATTTTTCTCATCCCATGAC
 TTCCCTCCGATGGT

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FIGURE 74

AGTATGAGGCGCCUACCCATGGTGGGATGGGACCGCGGGCTGCAGATGCTGCTGACCAAGGCCGGAGCCTTCGGC
GCCTTCTCGCTCATGSCCATCGCCATCGGCACCGACTACTGGCTGTACTCCAGCGCGGCACATCTGCACGGGCAC
CAACCTGACCATGGACGACGGGGCCCCCGCCCCGCGCGCCCGCGGGGACCTCACCCACTCTGGTCTGTGGCGGG
TGTGCTGCATCGAAGGGATCTATAAAGGGCACTGCTTCCGGATCAATCACTTCCCAGAGGACAATGACTACGAC
CAGGACAGCTCGGAGTACCTCCTCCGCATCGTGGGAGCCTCCAGCGTCTTCCCTATCCTCAGCACCATTCTGTCT
CCTGCTGGGTGGCCTGTGCATCGGTGCTGGCAGGATCTACAGCGCAAGAACAACATCGTCCCTCAGTCCCGCA
TCCTCTTCGTGGCTGCAGGCCTCAGTAACATCATCGGTATCATCGTCTACATTTCCAGCAACACAGGTGACCCG
AGTGACAAGCGGGACGAGACAAAGAACCAATTACAACTACGGCTGGTCTTTTACTTTGGAGCTCTGTCTTT
CATTTGTGGCTGAGACCGTGGGCGTCTTGGCTGTAAACATTTACATTGAGAAAATAAAGAGTTGAGCTTTAAGA
CCAAACGGGAATTCCTTAAGGCGTCTTCCTCTTCTCCTTATGCCAGGATGCCGAGCTACAGGTACCGCCGACGG
CGCTCGAGGTCCAGCTCAAGTCCACCGAGGCCCTCGCCCTCCAGGGACCTCTCGCCCATGGGCTGAAGATCAC
AGGGGCCATCCCCATGGGGGAGCTGTCCATGTACACGCTGTCCAGGGAGCCCCCTCAAGGTGACCACCGCAGCCA
GCTACAGCCCCGACCAGGAGGCCAGCTTCCTGCAGGTGCATGACTTTTCACACAGGACCTGAAGGAAGGTTTC
CACGTCAGCATGCTGAACCGACGAGGACCCCTGTCTGA